GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 31, 2001, 15:02:40 ; Search time 15.58 Seconds
(without alignments)
740.893 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 948
Sequence: 1 ADRERSIHDFCLVSKVVGRC.....ACMLRCFRQQENPPLPLGSK 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	658	69.4	252	2	JG0185	hepatocyte growth
2	250.5	26.4	1558	2	T34394	hypothetical prote
3	250.5	26.4	2167	2	T34395	hypothetical prote
4	249.5	26.3	352	1	TIBOBI	alpha-1-microglobu
5	246.5	26.0	302	1	TIRTGK	tissue factor path
6	244.5	25.8	123	2	A29652	inter-alpha-trypsi
7	244.5	25.8	352	1	HCHU	alpha-1-microglobu
8	244	25.7	299	2	I46937	tissue factor path
9	243	25.6	300	2	S12143	lipoprotein-associ
10	242.5	25.6	337	1	TIPGBI	alpha-1-microglobu
11	241.5	25.5	125	1	TIHOBI	alpha-1-microglobu
12	240	25.3	2225	2	T26063	hypothetical prote
13	239.5	25.3	396	2	S53325	tissue factor path
14	237.5	25.1	349	2	S21089	alpha-1-microglobu
15	236.5	24.9	304	1	JC2264	tissue factor path
16	235.5	24.8	349	2	S35708	alpha-1-microglobu
17	233.5	24.6	304	1	TIHUGK	tissue factor path
18	222	23.4	1043	2	T19734	hypothetical prote
19	219	23.1	922	2	T23573	hypothetical prote
20	214.5	22.6	235	2	A54951	tissue factor path
21	210	22.2	765	2	S42880	amyloid precursor-
22	209	22.0	1743	2	T26859	hypothetical prote
23	208	21.9	751	2	A49974	beta-amyloid precu
24	200	21.1	763	2	A49321	amyloid beta (A4)
25	200	21.1	1599	2	T16210	hypothetical prote
26	195	20.6	1391	2	T20406	hypothetical prote
27	193.5	20.4	111	2	S41082	amyloid precursor
28	193	20.4	2844	2	S28291	hypothetical prote
29	186.5	19.7	747	2	JH0773	Alzheimer's diseas
30	186	19.6	484	4	A32761	hypothetical [illegible]
31	186	19.6	770	1	QRHUA4	Alzheimer's [illegible]
32	185.5	19.6	1203	2	T21275	hypothetical [illegible]
33	181.5	19.1	355	1	S22181	gamma-1-microglo[illegible]
34	178	18.8	1965	2	T33216	hypothetical pr[illegible]
35	175.5	18.5	76	2	S03607	Alzheimer's d[illegible]
36	174.5	18.4	76	2	S04855	Alzheimer's d[illegible]
37	174.5	18.4	76	2	S06678	Alzheimer's [illegible]
38	174.5	18.4	100	2	A32282	Alzheimer's [illegible]
39	174.5	18.4	692	2	T32980	hypothetical pr[illegible]
40	167	17.6	62	2	S07451	proteinase inhibi[illegible]
41	164	17.3	838	2	T20125	hypothetical prote
42	163.5	17.2	372	2	JC2556	alpha-1-microglobu
43	161	17.0	1208	2	T27822	hypothetical prote
44	159	16.8	265	2	A53390	Kunitz-type protei
45	156	16.5	64	2	S41399	Kunitz-type protei

ALIGNMENTS

RESULT 1
JG0185
hepatocyte growth factor activator inhibitor type 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JG0185
R;Itoh, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Koono, M.
Biochem. Biophys. Res. Commun. 255, 740-748, 1999
A;Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first kunit
A;Reference number: JG0185; MUID:99160423
A;Accession: JG0185
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-252 <ITO>
A;Cross-references: GB:AF099016
C;Superfamily: animal Kunitz-type proteinase inhibitor homology
F;133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 69.4%; Score 658; DB 2; Length 252;
Best Local Similarity 68.2%; Pred. No. 7.6e-52;
Matches 116; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

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Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           | ||  :|: | ||||||:||||:|||||||:|||||| |||||||:|| ||| :||||| |
Db      28 ASRELDVHESCGVSKVVGKCRASIPRWWYNITDGSCQPFVYGGCEGNGNNYQSKEECLDK 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           || |||| | | | :|| ||||| | ||:| :|| |:::|||||||   |||||||:||
Db      88 CAGVTENTTDDNARNRNGADSSVLSVPRKQSAEDLSAEIFNYEEYCVPKAVTGPCRAAFP 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           |||:| |:||| :|||||||||||||| |:|||| | :| :| |  | |
Db     148 RWYYDTEKNSCISFIYGGCRGNKNSYLSQEACMQHCSGKQMHPFLTPGLK 197
```

RESULT 2
T34394
hypothetical protein C37C3.6a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34394
R;Geisel, C.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid C37C3.
A;Reference number: Z21518
A;Accession: T34394
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1558 <GEI>
A;Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6
A;Experimental source: strain Bristol N2; clone C37C3

```
C;Genetics:
A;Gene: CESP:C37C3.6a
A;Map position: 5
A;Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1

  Query Match           26.4%;  Score 250.5;  DB 2;  Length 1558;
  Best Local Similarity 30.1%;  Pred. No. 1.6e-14;
  Matches   49;  Conservative   26;  Mismatches   79;  Indels    9;  Gaps    1;

Qy       5 RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC--- 61
Db    1265 QSMEDICRSRQDAGPCETYSDQWFYNAFSQECETFTYGGCGGNLNRFRSKDECEQRCFFV 1324

Qy      62 ------ATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPC 115
Db    1325 HGAQPSAARQEQAQPAAQPAQPAQPSNIVSPPQQSASPVVVPSNSKQRDACHLNVDQGRC 1384

Qy     116 RASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFR 158
Db    1385 KGAFDSWYYEVATGSCVTFKYTGCGGNANRFASKDQCESLCVK 1427


RESULT   3
T34395
hypothetical protein C37C3.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34395
R;Geisel, C.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid C37C3.
A;Reference number: Z21518
A;Accession: T34395
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2167 <GEI>
A;Cross-references: EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN00023; CESP:C37C3.6b
A;Experimental source: strain Bristol N2; clone C37C3
C;Genetics:
A;Gene: CESP:C37C3.6b
A;Map position: 5
A;Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/

  Query Match           26.4%;  Score 250.5;  DB 2;  Length 2167;
  Best Local Similarity 30.1%;  Pred. No. 2.3e-14;
  Matches   49;  Conservative   26;  Mismatches   79;  Indels    9;  Gaps    1;

Qy       5 RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC--- 61
Db    1265 QSMEDICRSRQDAGPCETYSDQWFYNAFSQECETFTYGGCGGNLNRFRSKDECEQRCFFV 1324

Qy      62 ------ATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPC 115
Db    1325 HGAQPSAARQEQAQPAAQPAQPAQPSNIVSPPQQSASPVVVPSNSKQRDACHLNVDQGRC 1384

Qy     116 RASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFR 158
Db    1385 KGAFDSWYYEVATGSCVTFKYTGCGGNANRFASKDQCESLCVK 1427


RESULT   4
TIBOBI
alpha-1-microglobulin / inter-alpha-trypsin inhibitor precursor [validated] - bovine
N;Alternate names: BI-14 (inhibitory fragment of ITI); bikunin; ITI
C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Feb-1985 #sequence_revision 04-Feb-2000 #text_change 18-Aug-2000
C;Accession: S68149; A91717; A90685; S31219; A01209
R;Lindqvist, A.; Akerstroem, B.
Biochim. Biophys. Acta 1306, 98-106, 1996
A;Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liver
A;Reference number: S68149; MUID:96201710
A;Accession: S68149
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352 <LIN>
A;Cross-references: EMBL:U35642; NID:g1016297; PIDN:AAB07599.1; PID:g1016298
R;Hochstrasser, K.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte
A;Reference number: A91717; MUID:84133807
A;Accession: A91717
A;Molecule type: protein
A;Residues: 227-267,'L',269-273,'Q',275-297,'AF',300-329,'Q',331-345,'R',347-348 <HOC
R;Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte
A;Reference number: A90685; MUID:85225967
A;Accession: A90685
A;Molecule type: protein
A;Residues: 347-349 <HOC2>
R;Hochstrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the ..
A;Reference number: A91718; MUID:84133808
A;Contents: annotation; reactive sites
R;Castillo, G.M.; Templeton, D.M.
FEBS Lett. 318, 292-296, 1993
A;Title: Subunit structure of bovine ESF (extracellular-matrix stabilizing factor/a
A;Reference number: S31219; MUID:93178646
A;Accession: S31219
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-214,'X',216,'X',218-220 <CAS>
C;Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocali
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;35-188/Domain: lipocalin homology <LIP>
F;231-281/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;241/Inhibitory site: Leu (chymotrypsin, elastase) #status experimental
F;250/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;297/Inhibitory site: Arg (trypsin) #status experimental

  Query Match           26.3%;  Score 249.5;  DB 1;  Length 352;
  Best Local Similarity 32.4%;  Pred. No. 4.2e-15;
  Matches   48;  Conservative   16;  Mismatches   45;  Indels   39;  Gaps

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
Db     229 DSCQLDYSQGPCLGLFKRYFYNGTSMACETFLYGGCMGNGNNFLSEKECLQTCRTV---- 284

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
Db     285 ----------------------------------EACNLPIVQGPCRSYIQLWAFDAVK 309

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
Db     310 GKCVRFSYGGCKGNGNKFYSEKECKEYC 337


RESULT   5
TIRTGK
tissue factor pathway inhibitor precursor - rat
N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation i..
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000
C;Accession: JX0213
R;Enjyoji, K.; Emi, M.; Mukai, T.; Kato, H.
J. Biochem. 111, 681-687, 1992
A;Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).
A;Reference number: JX0213; MUID:92348361
A;Accession: JX0213
A;Molecule type: mRNA
A;Residues: 1-302 <ENJ>
```

A;Cross-references: DDBJ:D10926; NID:g220916; PIDN:BAA01724.1; PID:g220917
A;Experimental source: liver
C;Comment: This serine proteinase inhibitor regulates clotting by factor Xa-dependent in
C;Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-302/Product: tissue factor pathway inhibitor #status predicted <MAT>
F;53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;124-174/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;222-272/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;288-291/Region: heparin binding #status predicted
F;53-103,62-86,78-99,124-174,133-157,149-170,222-272,231-255,247-268/Disulfide bonds: #s
F;63/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predict
F;134/Inhibitory site: Arg (coagulation factor X) #status predicted
F;144,251,261/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;232/Inhibitory site: Lys (unidentified proteinase) #status predicted

Query Match 26.0%; Score 246.5; DB 1; Length 302;
Best Local Similarity 34.0%; Pred. No. 6.7e-15;
Matches 54; Conservative 21; Mismatches 65; Indels 19; Gaps 3;

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Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCA-TVTEN 67
           ||| : :  | ||  | |::||     |: | |||| ||||| : | |||   |   | |
Db     122 DFCFLEEDPGICRGFMTRYFYNNQSKQCEQFKYGGCLGNSNNFETLEECRNTCEDPVNEV 181

Qy      68 ATGDLATSR----------NAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRA 117
             ||  |::          |          || : | :  |        :|   | :| |:|
Db     182 QKGDYVTNQITVTDRTTVNNVVIPQATKAPSQWDYDGPS--------WCLEPADSGLCKA 233

Qy     118 SFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           |  |:|::    |  | | || || |:: ::: |   |
Db     234 SEKRFYYNPAIGKCRQFNYTGCGGNNNNFTTKQDCNRAC 272
```

RESULT 6
A29652
inter-alpha-trypsin inhibitor (BPI type) - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jul-1999
C;Accession: A29652
R;Rasp, G.; Hochstrasser, K.; Wachter, E.; Reisinger, P.W.M.
Biol. Chem. Hoppe-Seyler 368, 727-731, 1987
A;Title: The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alph
sin inhibitor, XI.).
A;Reference number: A29652; MUID:87299012
A;Accession: A29652
A;Molecule type: protein
A;Residues: 1-123 <RAS>
C;Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocalin h
C;Keywords: serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;61-111/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Query Match 25.8%; Score 244.5; DB 2; Length 123;
Best Local Similarity 31.8%; Pred. No. 4e-15;
Matches 47; Conservative 15; Mismatches 47; Indels 39; Gaps 1;

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Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |     |::|| |  :|: | |||| || ||: :::|||: | ||
Db       3 DSCQLGYSQGPCLGMFKRYFYNGTSMACETFYYGGCMGNGNNFPSEKECLQTCRTV---- 58

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                    : |    | |||||    | ||  :
Db      59 ----------------------------------QACNLPIVRGPCRAGIELWAFDAVK 83

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           |  |||||| || | : |:: |   |
Db      84 GKCVRFIYGGCNGNGNQFYSQKECKEYC 111
```

RESULT 7
HCHU
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - human
N;Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC
rich protein
N;Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1982 #sequence_revision 30-Jun-1987 #text_change 04-Feb-2000
C;Accession: S13433; S10778; A93642; A90074; A90225; A90686; PN0450; B39079; A61580;
3217
R;Vetr, H.; Gebhard, W.
Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
A;Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
A;Reference number: S13433; MUID:91214554
A;Accession: S13433
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <VET1>
A;Cross-references: EMBL:X54816; NID:g24475; PIDN:CAA38585.1; PID:g825614; EMBL:X549
R;Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Salier, J.P.; Leveillard, T.; M
Eur. J. Biochem. 191, 131-139, 1990
A;Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain g
A;Reference number: S10778; MUID:90336621
A;Accession: S10778
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-202 <DIA>
R;Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
Nucleic Acids Res. 14, 7839-7850, 1986
A;Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-
A;Reference number: A93642; MUID:87040757
A;Accession: A93642
A;Molecule type: mRNA
A;Residues: 1-352 <KAU>
A;Cross-references: GB:X04494; NID:g24478; PIDN:CAA28182.1; PID:g24479
R;Lopez Otin, C.; Grubb, A.O.; Mendez, E.
Arch. Biochem. Biophys. 228, 544-554, 1984
A;Title: The complete amino acid sequence of human complex-forming glycoprotein
A;Reference number: A90074; MUID:84126849
A;Accession: A90074
A;Molecule type: protein
A;Residues: 20-56,58-202 <LOP>
A;Experimental source: individual with tubular proteinuria
A;Note: no evidence of sequence heterogeneity could be found, in spite of persist
R;Takagi, T.; Takagi, K.; Kawai, T.
Biochem. Biophys. Res. Commun. 98, 997-1001, 1981
A;Title: Complete amino acid sequence of human alpha--1-microglobulin.
A;Reference number: A90225; MUID:81184038
A;Accession: A90225
A;Molecule type: protein
A;Residues: 20-47;58-136,138-141,'T',143-144,146-198 <TAK>
A;Experimental source: pooled urine of patients with tubular proteinuria
R;Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempart, K.; Salier, J.-
Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
A;Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type
A;Reference number: A90686; MUID:85225968
A;Accession: A90686
A;Molecule type: protein
A;Residues: 206-290,'VI',293-342,'E',344-350 <REI>
R;Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Drueeke, T.; Daudon, M.
Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
A;Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor
A;Reference number: PN0450; MUID:93221481
A;Accession: PN0450
A;Molecule type: protein
A;Residues: 206-214,'X' <ATM1>
R;Enghild, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherfurd, S.; Pizzo, S
J. Biol. Chem. 266, 747-751, 1991
A;Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood p
A;Reference number: A39079; MUID:91093267
A;Accession: B39079
A;Molecule type: protein
A;Residues: 206-225 <ENG1>

R;Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
Int. J. Biochem. 23, 1201-1203, 1991
A;Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inhi
A;Reference number: A61580; MUID:92175157
A;Accession: A61580
A;Molecule type: protein
A;Residues: 214,'X',216-222,'X' <CHI>
R;McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.
J. Biol. Chem. 261, 5378-5383, 1986
A;Title: Two apparent human endothelial cell growth factors from human hepatoma cells ar
A;Reference number: A92583; MUID:86168278
A;Accession: B25604
A;Molecule type: protein
A;Residues: 206-214,'X',216-230,'X',232-239,'X',241-248,'XX',251-252,'X',254 <MCK>
R;Enghild, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.
J. Biol. Chem. 264, 15975-15981, 1989
A;Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
A;Reference number: A92736; MUID:89380192
A;Accession: C34245
A;Molecule type: protein
A;Residues: 206-225 <ENG2>
A;Traboni, C.; Cortese, R.
Nucleic Acids Res. 14, 6340, 1986
A;Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobul
A;Reference number: A25303; MUID:86312901
A;Accession: A25303
A;Molecule type: mRNA
A;Residues: 1-218,'HW' <TRA>
A;Note: this mRNA sequence appears to contain errors after residue 218
R;Calero, M.; Escribano, J.; Grubb, A.; Mendez, E.
J. Biol. Chem. 269, 384-389, 1994
A;Title: Location of a novel type of interpolypeptide chain linkage in the human protein
A;Reference number: A53110; MUID:94103241
A;Accession: A53110
A;Molecule type: protein
A;Residues: 45-57 <CAL1>
R;Vetr, H.; Koegler, M.; Gebhard, W.
FEBS Lett. 245, 137-140, 1989
A;Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inhi
A;Reference number: S03552; MUID:89171290
A;Accession: S03552
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 206-352 <VET2>
R;Malki, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fourne
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
A;Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation
A;Reference number: S28928; MUID:93039735
A;Accession: S28930
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-215 <MAL>
R;Morelle, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michalski, C.; Fournet
Eur. J. Biochem. 221, 881-888, 1994
A;Title: Chondroitin sulphate covalently cross-links the three polypeptide chains of int
A;Reference number: S43466; MUID:94229087
A;Accession: S43466
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-221 <MOR>
R;Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
Biochemistry 33, 7423-7429, 1994
A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable compl
A;Reference number: A53642; MUID:94271799
A;Accession: A53642
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-217 <WIS>
R;Calero, M.; Mendez, E.; Garcia, E.
Biochim. Biophys. Acta 1249, 91-99, 1995
A;Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin)
A;Reference number: S55688; MUID:95284116
A;Accession: S55688
A;Molecule type: protein
A;Residues: 20-24 <CAL2>
R;Bourguignon, J.; Diarra-Mehrpour, M.; Sesboue, R.; Frain, M.; Sala-Trepat, J.M.; Ma
Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
A;Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide
A;Reference number: I52208; MUID:86025577
A;Accession: I52208
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 302-352 <BOU>
A;Cross-references: GB:M11562; NID:g186587; PIDN:AAA59194.1; PID:g307077
R;Wojcik, E.G.C.; van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Re
Biochem. J. 311, 753-759, 1995
A;Title: Factor IX Zutphen: a Cys(18) -> Arg mutation results in formation of a heter
A;Reference number: S59509; MUID:96067589
A;Accession: S59509
A;Molecule type: protein
A;Residues: 27-35,'Y',37 <WOJ>
R;Atmani, F.; Mizon, J.; Khan, S.R.
Eur. J. Biochem. 236, 984-990, 1996
A;Title: Identification of uronic-acid-rich protein as urinary bikunin, the light cha
A;Reference number: S66434; MUID:96270753
A;Accession: S66434
A;Molecule type: protein
A;Residues: 206-214,'X',216-230 <ATM2>
R;Akerstroem, B.; Bratt, T.; Enghild, J.J.
FEBS Lett. 362, 50-54, 1995
A;Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect
A;Reference number: S68728; MUID:95212582
A;Accession: S68728
A;Molecule type: protein
A;Residues: 89-100 <AKE>
R;Jessen, T.E.; Faarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A;Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor
A;Reference number: S02431; MUID:88167187
A;Accession: S02431
A;Molecule type: protein
A;Residues: 206-214,'X',216-217 <JES>
R;Lopez, C.; Grubb, A.; Mendez, E.
FEBS Lett. 144, 349-353, 1982
A;Title: Human protein HC displays variability in its carboxyl-terminal amino acid se
A;Reference number: A91304
A;Contents: annotation; variant of alpha-1-microglobulin
A;Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys
R;Hochstrasser, K.; Schonberger, O.L.; Rossmanith, I.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the in
by affinity chromatography.
A;Reference number: A91698; MUID:82074265
A;Contents: annotation; carbohydrate binding sites
R;Morii, M.; Travis, J.
Biol. Chem. Hoppe-Seyler 366, 19-21, 1985
A;Title: The reactive site of human inter-alpha-trypsin inhibitor is in the ar
A;Reference number: A90682; MUID:85225940
A;Contents: annotation; inhibitory site
A;Note: in vitro, the first twelve residues of the amino end of the inhibitor
wn
C;Comment: Alpha-1-microglobulin and inter-alpha-trypsin inhibitor are proteolytic
C;Comment: Alpha-1-microglobulin occurs in many physiological fluids including b
. It contains at least one brown-yellow chromophore.

Query Match 25.8%; Score 244.5; DB 1; Length 352;
Best Local Similarity 32.4%; Pred. No. 1.2e-14;
Matches 48; Conservative 14; Mismatches 47; Indels 39; Gaps 1;

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Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |     |::|| |  :|: | |||| || ||::|::|||: | ||
Db     229 DSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRTVAA-- 286

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          |    | |||||    | ||  :
Db     287 ------------------------------------CNLPIVRGPCRAFIQLWAFDAVK 309
```

```
Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           |  | ||||:|| | : ||: |   |
Db     310 GKCVLFPYGGCQGNGNKFYSEKECREYC 337
```

RESULT 8
I46937
tissue factor pathway inhibitor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C;Accession: I46937
R;Belaaouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 1993
A;Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A;Reference number: I46937; MUID:93276427
A;Accession: I46937
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-299 <BEL>
A;Cross-references: GB:S61902; NID:g386015; PIDN:AAB26836.1; PID:g386016
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F;49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>
F;120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>

Query Match 25.7%; Score 244; DB 2; Length 299;
Best Local Similarity 30.0%; Pred. No. 1.1e-14;
Matches 48; Conservative 23; Mismatches 61; Indels 28; Gaps 2;

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Qy       4 ERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCAT 63
           ::  | ||  :    | ||| : |:::|:    |: |:||||:|| | : : ||| :|||
Db      42 QKPTHSFCAMKVDDGPCRAYIKRFFFNILTHQCEEFIYGGCEGNENRFESLEECKEKCAR 101

Qy      64 VTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWY 123
               |  |   :  |                          :|      | ||    |::
Db     102 DYPKMTTKLTFQKGKPD----------------------FCFLEEDPGICRGYITRYF 137

Qy     124 FDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 163
           ::  :   |  | |||| || |:: | | |   |    |||
Db     138 YNNQSKQCERFKYGGCLGNLNNFESLEECKNTC----ENP 173
```

RESULT 9
S12143
lipoprotein-associated coagulation inhibitor precursor - rabbit
N;Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C;Accession: S12143; A61373
R;Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
Nucleic Acids Res. 18, 6440, 1990
A;Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.
A;Reference number: S12143; MUID:91057146
A;Accession: S12143
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-300 <WES>
A;Cross-references: EMBL:X54708; NID:g1612; PIDN:CAA38515.1; PID:g1613
R;Colburn, P.; Crabb, J.W.; Buonassisi, V.
J. Cell. Physiol. 148, 320-326, 1991
A;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cel
A;Reference number: A61373; MUID:91349227
A;Accession: A61373
A;Molecule type: protein
A;Residues: 25-33,'X',35-46 <COL>
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; glycoprotein
F;50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match 25.6%; Score 243; DB 2; Length 300;
Best Local Similarity 30.0%; Pred. No. 1.4e-14;
Matches 48; Conservative 23; Mismatches 61; Indels 28; Gaps 2;

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Qy       4 ERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCAT 63
           ::  | ||  :    | ||| : |:::|:    |: |:||||:|| | : : ||| :|||
Db      43 QKPTHSFCAMKVDDGPCRAYIKRFFFNILAHQCEEFIYGGCEGNENRFESLEECKEKCAR 102

Qy      64 VTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWY 123
               |  |   :  |                          :|      | ||    |::
Db     103 DYPKMTTKLTFQKGKPD----------------------FCFLEEDPGICRGYITRYF 138

Qy     124 FDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 163
           ::  :   |  | |||| || |:: | | |   |    |||
Db     139 YNNQSKQCERFKYGGCLGNLNNFESLEECKNTC----ENP 174
```

RESULT 10
TIPGBI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - pig (fragment)
N;Alternate names: bikunin; ITI; PI-14 (inhibitory fragment of ITI)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: S11066; S13493; A01208
R;Gebhard, W.; Schreitmueller, T.; Vetr, H.; Wachter, E.; Hochstrasser, K.
FEBS Lett. 269, 32-36, 1990
A;Title: Complementary DNA and deduced amino acid sequences of porcine alpha1-microgl
A;Reference number: S11066; MUID:90353595
A;Accession: S11066
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-337 <GEB>
A;Cross-references: EMBL:X53685; NID:g1877; PIDN:CAA37725.1; PID:g1878
R;Tavakkol, A.
Biochim. Biophys. Acta 1088, 47-56, 1991
A;Title: Molecular cloning of porcine alpha(1)-microglobulin/HI-30 reveals developmen
A;Reference number: S13493; MUID:91113729
A;Accession: S13493
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'M',3-48,'M',50-337 <TAV>
A;Cross-references: GB:X52087; NID:g1881; PIDN:CAA36306.1; PID:g1882
A;Note: the authors translated the codon GTG for residue 2 as a Met initiation codon
R;Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte
A;Reference number: A90685; MUID:85225967
A;Accession: A01208
A;Molecule type: protein
A;Residues: 212-258,'Q',260-269,'S',271-277,'Q',279-282,'A',284,'IR',287-292,'A',294-
C;Comment: This inhibitory fragment, released from native ITI after limited proteolys
first domain interacts weakly with PMN-granulocytic elastase and not at all with panc
C;Comment: The amino acid at position P2' (228-Met) appears to determine the specific
nd elastase; those with leucine interact strongly.
C;Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocal
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;20-173/Domain: lipocalin homology <LIP>
F;216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;272-322/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;216-266,225-249,241-262,272-322,281-305,297-318/Disulfide bonds: #status pred
F;226/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F;235/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;282/Inhibitory site: Arg (trypsin) #status predicted

Query Match 25.6%; Score 242.5; DB 1; Length 337;
Best Local Similarity 31.8%; Pred. No. 1.7e-14;
Matches 47; Conservative 19; Mismatches 43; Indels 39; Gaps 4;

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Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    |  |   : |::|| :  :|: | |||| || ||:::::|||: | ||
Db     214 DSCQLGYSQGPCLGMIKRYFYNGSSMACETFHYGGCMGNGNNFVSEKECLQTCRTV---- 269
```

```
Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          | |:   |:|||| |  | ||  :
Db     270 ----------------------------------EACSLPIVSGPCRGFFQLWAFDAVQ 294

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           |  | ||||:|| | : ||: |   |
Db     295 GKCVLFNYGGCQGNGNQFYSEKECKEYC 322


RESULT  11
TIHOBI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
N;Alternate names: EI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI
C;Species: Equus caballus (domestic horse)
C;Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 05-May-2000
C;Accession: A01210; A45653
R;Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A;Reference number: A90685; MUID:85225967
A;Accession: A01210
A;Molecule type: protein
A;Residues: 3-125 <HOC>
R;Veeraragavan, K.; Singh, K.; Wachter, E.; Hochstrasser, K.
Biochem. Int. 26, 405-413, 1992
A;Title: Characterization of a trypsin inhibitor from equine urine.
A;Reference number: A45653; MUID:92328813
A;Accession: A45653
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12,'E',14-33 <VEE>
A;Cross-references: PIDN:AAB22430.1; PID:g250858
A;Experimental source: urine
A;Note: sequence extracted from NCBI backbone (NCBIP:107966)
C;Comment: This inhibitory fragment, released from native ITI after limited proteolysis
first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
C;Comment: The amino acid at position P2' (19-Met) appears to determine the specificity
d elastase; those with leucine interact strongly.
C;Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocalin h
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
F;17/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F;26/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;73/Inhibitory site: Arg (trypsin) #status predicted

  Query Match           25.5%;  Score 241.5;  DB 1;  Length 125;
  Best Local Similarity   31.8%;  Pred. No. 7.5e-15;
  Matches   47;  Conservative   15;  Mismatches   47;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |   : |::|| |  :|: | |||| || ||: :::|||: | ||
Db       5 DSCQLDHAQGPCLGMISRYFYNGTSMACETFQYGGCLGNGNNFASQKECLQTCRTVAA-- 62

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          |    | |||||    | ||  :
Db      63 ----------------------------------CNLPIVQGPCRAFIRLWAFDAAQ 85

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           |  | |||||||  | : |:: |   |
Db      86 GKCVLFTYGGCRGNGNKFYSQKECKEYC 113


RESULT  12
T26063
hypothetical protein W01F3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26063
R;Cummings, P.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z20145
A;Accession: T26063
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2225 <WIL>
A;Cross-references: EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
A;Experimental source: clone W01F3
C;Genetics:
A;Gene: CESP:W01F3.3
A;Map position: 5
A;Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; ...

  Query Match           25.3%;  Score 240;  DB 2;  Length 2225;
  Best Local Similarity   29.3%;  Pred. No. 2.1e-13;
  Matches   46;  Conservative   21;  Mismatches   58;  Indels   32;  Gaps    2;

Qy      11 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC--ATVTENA 69
           ||  :  | ||    ||:::    :| :| | || || ||: :|||||:  |     | :|
Db     777 CLHPRDSGNCRGQFVRWFFDDEKKNCDVFTYTGCQGNGNNFASKEECMAICHKPEPTPSA 836

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
           | |                                : : |: :   | |   | |: || |
Db     837 TPD----------------------------FSQVCSNDVDAGECNGVFERFAFDADA 880

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPL 165
             |  | |||| || |:: : : |  ||    :  |:
Db     867 QDCRAFTYGGCGGNGNNFATMQECRSRCVMAMKKSPV 903


RESULT  13
S53325
tissue factor pathway inhibitor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 16-Jul-1999
C;Accession: S53325
R;Girard, T.J.; Gailani, D.; Broze Jr., G.J.
Biochem. J. 303, 923-928, 1994
A;Title: Complementary DNA sequencing of canine tissue factor pathway inhibitor revea
A;Reference number: S53325; MUID:95071310
A;Accession: S53325
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-396 <GIR>
C;Superfamily: animal Kunitz-type proteinase inhibitor homology
C;Keywords: serine proteinase inhibitor
F;53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;309-359/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

  Query Match           25.3%;  Score 239.5;  DB 2;  Length 396;
  Best Local Similarity   29.6%;  Pred. No. 3.8e-14;
  Matches   45;  Conservative   24;  Mismatches   60;  Indels   23;  Gaps    1;

Qy       5 RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATV 64
           | :| || :    | ||| :  :::|:    |: |:||||:|| | : : ||| :|| |
Db      47 RLLHSFCALKADNGPCRAMIRNYFFNIHTQQCEEFIYGGCEGNQNRFESLEECEEKCVRV 106

Qy      65 TENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124
             |                                :    :    :|| |  :| ||    |:|:
Db     107 YPKA----------------------KTETLEKVLEKPDYCHMNEDSGLCRGFVTRYYY 143

Qy     125 DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           :   : |  | |||| || |:: : | |   |
Db     144 NNVSSKCEGFKYGGCLGNLNNFETLEQCKNTC 175


RESULT  14
S21089
alpha-1-microglobulin/inter-alpha-trypsin inhibitor light chain precursor - rat
N;Alternate names: acid-stable proteinase inhibitor; bikunin; trypstatin
```

C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C;Accession: S21089; A53056; A25935; A31890; A61633
R;Lindqvist, A.; Bratt, T.; Altieri, M.; Kastern, W.; Akerstroem, B.
Biochim. Biophys. Acta 1130, 63-67, 1992
A;Title: Rat alpha(1)-microglobulin: co-expression in liver with the light chain of inte
A;Reference number: S21089; MUID:92182014
A;Accession: S21089
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-349 <LIN>
A;Cross-references: GB:S87544; NID:g247162; PIDN:AAB21782.1; PID:g247163
R;Itoh, H.; Ide, H.; Ishikawa, N.; Nawa, Y.
J. Biol. Chem. 269, 3818-3822, 1994
A;Title: Mast cell protease inhibitor, trypstatin, is a fragment of inter-alpha-trypsin
A;Reference number: A53056; MUID:94148892
A;Accession: A53056
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 285-341 <ITO>
R;Kastern, W.; Bjorck, L.; Akerstrom, B.
J. Biol. Chem. 261, 15070-15074, 1986
A;Title: Developmental and tissue-specific expression of alpha-1-microglobulin mRNA in t
A;Reference number: A25935; MUID:87033744
A;Accession: A25935
A;Molecule type: protein
A;Residues: 141,'A',143-195 <KAS>
R;Kido, H.; Yokogoshi, Y.; Katunuma, N.
J. Biol. Chem. 263, 18104-18107, 1988
A;Title: Kunitz-type protease inhibitor found in rat mast cells. Purification, propertie
A;Reference number: A31890; MUID:89053978
A;Accession: A31890
A;Molecule type: protein
A;Residues: 283-301,'L',303-322,'N',324-329,'PK',332-333,'W',335-343 <KID>
R;Sugiki, M.; Maruyama, M.; Yoshida, E.; Sumi, H.; Mihara, H.
Inflammation 15, 281-289, 1991
A;Title: Acid-stable protease inhibitor in chronic phase of carrageenin-induced inflamma
A;Reference number: A61633; MUID:92120777
A;Accession: A61633
A;Molecule type: protein
A;Residues: 205-213,'X',215-229,'N',231-232,'K',234-238 <SUG>
C;Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocalin h
C;Keywords: chondroitin sulfate proteoglycan; chromoprotein; glycoprotein; plasma; serin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-202/Product: alpha-1-microglobulin #status predicted <A1M>
F;34-187/Domain: lipocalin homology <LIP>
F;205-349/Product: inter-alpha-trypsin inhibitor #status experimental <IAI>
F;230-280/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;286-336/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;24/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;52/Cross-link: alpha-1-microglobulin-Ig alpha complex chromophore (Cys) (interchain to
F;114,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;214/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
F;296/Inhibitory site: Arg (trypsin) #status predicted

Query Match 25.1%; Score 237.5; DB 2; Length 349;
Best Local Similarity 30.4%; Pred. No. 5e-14;
Matches 45; Conservative 17; Mismatches 47; Indels 39; Gaps 1;

```
Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | ::   | |     :::||    :|: | |||| || ||: :::|||: | |:
Db     228 DSCQLNYSEGPCLGMQQKYYYNGASMACETFQYGGCLGNGNNFASEKECLQTCRTIAA-- 285

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          |   | |||||    | ||  :
Db     286 -----------------------------------CNLPIVQGPCRAFAELWAFDAAQ 308

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  ||||||:|| | : ||: |   |
Db     309 GKCIQFIYGGCKGNGNKFYSEKECKEYC 336
```

RESULT 15
JC2264
tissue factor pathway inhibitor precursor - rhesus macaque
N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation i
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: JC2264
R;Kamei, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miy
J. Biochem. 115, 708-714, 1994
A;Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor
A;Reference number: JC2264; MUID:94375417
A;Accession: JC2264
A;Molecule type: mRNA
A;Residues: 1-304 <KAM>
A;Cross-references: GB:S73337; NID:g685016; PIDN:AAB31955.1; PID:g685017
A;Experimental source: liver
C;Comment: This protein inhibits the activities of factor Xa and tissue factor-fac
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhib
C;Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;54-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds
F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status pred
F;135/Inhibitory site: Arg (coagulation factor X) #status predicted
F;145,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 24.9%; Score 236.5; DB 1; Length 304;
Best Local Similarity 34.9%; Pred. No. 5.3e-14;
Matches 53; Conservative 24; Mismatches 64; Indels 11; Gaps 4;

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Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           ||| : :  | ||  : |::||     |: | |||| || ||: | |||   |   :
Db     123 DFCFLEEDPGICRGYITRYFYNNQSKQCERFKYGGCLGNMNNFETLEECKNTC---EDGI 179

Qy      69 TG----DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124
           |     :  |  || ::|    |  | ::  |   |:    :| | |  | |||:  |:|:
Db     180 NGFQVDNYGTQLNAVNNS--QTP--QSTKVPSFFEFHGPSWCLAPADRGLCRANENRFYY 235

Qy     125 DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           :     |  | | || ||:|:: |:  |:  |
Db     236 NSVIGKCRPFKYSGCGGNENNFTSKRECLRAC 267
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Search completed: January 31, 2001, 15:03:23
Job time: 43 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 31, 2001, 15:03:08 ; Search time 10.15 Seconds
(without alignments)
540.886 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 948
Sequence: 1 ADRERSIHDFCLVSKVVGRC.....ACMLRCFRQQENPPLPLGSK 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	249.5	26.3	352	1	AMBP_BOVIN	P00978 bos taurus
2	247.5	26.1	346	1	AMBP_MERUN	Q62577 meriones un
3	246.5	26.0	302	1	TFPI_RAT	Q02445 rattus norv
4	244.5	25.8	123	1	IATR_SHEEP	P13371 ovis aries
5	244.5	25.8	352	1	AMBP_HUMAN	P02760 homo sapien
6	244	25.7	300	1	TFPI_RABIT	P19761 oryctolagus
7	242.5	25.6	337	1	AMBP_PIG	P04366 sus scrofa
8	241.5	25.5	123	1	IATR_HORSE	P04365 equus cabal
9	237.5	25.1	349	1	AMBP_RAT	Q64240 rattus norv
10	236.5	24.9	304	1	TFPI_MACMU	Q28864 macaca mula
11	235.5	24.8	349	1	AMBP_MESAU	Q60559 mesocricetu
12	235.5	24.8	349	1	AMBP_MOUSE	Q07456 mus musculu
13	233.5	24.6	304	1	TFPI_HUMAN	P10646 homo sapien
14	214.5	22.6	235	1	TFP2_HUMAN	P48307 homo sapien
15	210	22.2	765	1	APP2_RAT	P15943 rattus norv
16	200	21.1	763	1	APP2_HUMAN	Q06481 homo sapien
17	191	20.1	1416	1	YN81_CAEEL	Q03610 caenorhabdi
18	187.5	19.8	770	1	A4_RAT	P08592 rattus norv
19	186	19.6	751	1	A4_SAISC	Q95241 saimiri sci
20	186	19.6	770	1	A4_HUMAN	P05067 homo sapien
21	183.5	19.4	770	1	A4_MOUSE	P12023 mus musculu
22	181.5	19.1	355	1	AMBP_PLEPL	P36992 pleuronecte
23	175.5	18.5	69	1	CRPT_BOOMI	P81162 boophilus m
24	174.5	18.4	76	1	A4_MACMU	P29216 macaca mula
25	174.5	18.4	87	1	A4_MACFA	P53601 macaca fasc
26	167	17.6	62	1	IP52_ANESU	P10280 anemonia su
27	159	16.8	265	1	TKD1_SHEEP	Q29428 ovis aries
28	156	16.5	64	1	KIB9_HUMAN	P49223 homo sapien
29	156	16.5	164	1	TKD1_BOVIN	Q28201 bos taurus
30	155	16.4	60	1	IBPS_BOVIN	P00975 bos taurus
31	155	16.4	100	1	BPT2_BOVIN	P04815 bos taurus
32	153	16.1	61	1	IBPI_TACTR	P16044 tachypleus
33	152.5	16.1	100	1	BPT1_BOVIN	P00974 bos taurus
34	152	16.0	65	1	IVB3_VIPAA	P00992 vipera ammo
35	150.5	15.9	60	1	IVB2_DABRU	P00990 daboia russ
36	150.5	15.9	122	1	UPTI_PIG	Q29100 sus scrofa
37	150	15.8	110	1	IBP_CARCR	P00993 caretta car
38	149	15.7	61	1	IVB1_VIPAA	P00991 vipera ammo
39	147	15.5	58	1	ISIK_HELPO	P00994 helix pomat
40	147	15.5	67	1	IBPC_BOVIN	P00976 bos taurus
41	145	15.3	55	1	ISH2_STOHE	P81129 stoichactis
42	145	15.3	62	1	IVBT_ERIMA	P24541 eristocophi
43	143	15.1	83	1	ELAC_MACEU	O62845 macropus eu
44	142	15.0	3137	1	CA36_CHICK	P15989 gallus gall
45	141	14.9	65	1	IVB1_BUNFA	P25660 bungarus fa

ALIGNMENTS

RESULT 1
AMBP_BOVIN
ID AMBP_BOVIN STANDARD; PRT; 352 AA.
AC P00978; P35420; Q28020;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN; INTER-alpha-
DE TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30) (BI-14)
DE (CUMULUS EXTRACELLULAR MATRIX STABILIZING FACTOR) (ESF)].
GN AMBP OR ITIL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96201710; PubMed=8611630;
RA Lindqvist A., Aakerstroem B.;
RT "Bovine alpha 1-microglobulin/bikunin. Isolation and characterization
RT of liver cDNA and urinary alpha 1-microglobulin.";
RL Biochim. Biophys. Acta 1306:98-106(1996).
RN [2]
RP SEQUENCE OF 227-349.
RX MEDLINE=85225967; PubMed=2408637;
RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
RT the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
RT trypsin-released inhibitors from horse and pig inter-alpha-trypsin
RT inhibitors.";
RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
RN [3]
RP SEQUENCE OF 227-348.
RX MEDLINE=84133807; PubMed=6199275;
RA Hochstrasser K., Wachter E.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
RT the inter-alpha-trypsin inhibitor, VII. Determination of the
RT amino-acid sequence of the trypsin-released inhibitor from bovine
RT inter-alpha-trypsin inhibitor.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:1679-1687(1983).
RN [4]
RP SEQUENCE OF 206-219.
RC TISSUE=FETAL SERUM;
RX MEDLINE=92291130; PubMed=1376324;
RA Chen L., Mao S.J.T., Larsen W.J.;
RT "Identification of a factor in fetal bovine serum that stabilizes the
RT cumulus extracellular matrix. A role for a member of the inter-alpha-
RT trypsin inhibitor family.";
RL J. Biol. Chem. 267:12380-12386(1992).
RN [5]
RP REACTIVE SITES.
RX MEDLINE=84133808; PubMed=6199276;
RA Hochstrasser K., Albrecht G.J., Schoenberger O.L., Wachter E.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
RT the inter-alpha-trypsin inhibitor, VII. Characterization of the

```
RT   bovine inhibitor as double-headed trypsin-elastase inhibitor.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:1689-1696(1983).
CC   -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC       FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC       APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC       AND ALBUMIN.
CC   -!- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
CC       URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC       ELASTASE.
CC   -!- FUNCTION: MAY DIFFUSE INTO FOLLICULAR FLUID AFTER AN OVULATORY
CC       STIMULUS TO ACT AS STRUCTURAL LINKER THAT ENSURE NORMAL CUMULUS
CC       EXPANSION, THROUGH STABILIZATION OF THE CUMULUS EXTRACELLULAR
CC       MATRIX THUS SUPPORTING THE PROCESS OF OVULATION.
CC   -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC       SEPARATELY FUNCTIONING PROTEINS.
CC   -!- PTM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE.
CC   -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC       FAMILY.
CC   -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ
CC       FAMILY OF INHIBITORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U35642; AAB07599.1; -.
DR   PIR; A01209; TIBOBI.
DR   HSSP; P10646; 1ADZ.
DR   INTERPRO; IPR000566; -.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR002345; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PFAM; PF00061; lipocalin; 1.
DR   PRINTS; PR00179; LIPOCALIN.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR   PROSITE; PS00213; LIPOCALIN; 1.
KW   Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
KW   Lipocalin.
FT   SIGNAL       1    19       BY SIMILARITY.
FT   CHAIN       20   203       ALPHA-1 MICROGLOBULIN.
FT   CHAIN      206   352       INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
FT                              CHAIN.
FT   BINDING     53    53       CHROMOPHORE (BY SIMILARITY).
FT   DOMAIN     227   282       I.
FT   DOMAIN     283   348       II.
FT   DISULFID    91   188       BY SIMILARITY.
FT   DISULFID   231   281       BY SIMILARITY.
FT   DISULFID   240   264       BY SIMILARITY.
FT   DISULFID   256   277       BY SIMILARITY.
FT   DISULFID   287   337       BY SIMILARITY.
FT   DISULFID   296   320       BY SIMILARITY.
FT   DISULFID   312   333       BY SIMILARITY.
FT   ACT_SITE   241   242       INHIBITORY SITE (P1) (CHYMOTRYPSIN,
FT                              ELASTASE).
FT   ACT_SITE   297   298       INHIBITORY SITE (P1) (TRYPSIN).
FT   CARBOHYD   115   115       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   223   223       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   250   250       N-LINKED (GLCNAC. . .).
FT   CONFLICT   209   209       T -> G (IN REF. 4).
FT   CONFLICT   217   217       A -> D (IN REF. 4).
FT   CONFLICT   268   268       G -> L (IN REF. 2 AND 3).
FT   CONFLICT   274   274       E -> Q (IN REF. 2 AND 3).
FT   CONFLICT   298   299       SY -> AF (IN REF. 2 AND 3).
FT   CONFLICT   330   330       E -> Q (IN REF. 2 AND 3).
FT   CONFLICT   346   346       E -> R (IN REF. 2 AND 3).
FT   CARBOHYD    18    18       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   352 AA;  39235 MW;  ED31C5CA02E70B19 CRC64;
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 Query Match          26.3%;  Score 249.5;  DB 1;  Length 352;
 Best Local Similarity  32.4%;  Pred. No. 3.9e-16;
 Matches  48;  Conservative  16;  Mismatches  45;  Indels  39;  Gaps  1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    |:|     |::|| |  :|: |:|||| || ||:|:::|||: | ||
Db     229 DSCQLDYSQGPCLGLFKRYFYNGTSMACETFLYGGCMGNGNNFLSEKECLQTCRTV---- 284

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                | |    | ||||:    | ||  :
Db     285 ----------------------------------EACNLPIVQGPCRSYIQLWAFDAVK 309

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     310 GKCVRFSYGGCKGNGNKFYSEKECKEYC 337


RESULT   2
AMBP_MERUN
ID   AMBP_MERUN      STANDARD;      PRT;   346 AA.
AC   Q62577; Q62576;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN; INTER-ALPHA-
DE   TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30)].
GN   AMBP OR ITIL.
OS   Meriones unguiculatus (Mongolian jird).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=95110820; PubMed=7529051;
RA   Ide H., Itoh H., Nawa Y.;
RT   "Sequencing of cDNAs encoding alpha 1-microglobulin/bikunin of
RT   Mongolian gerbil and Syrian golden hamster in comparison with man and
RT   other species.";
RL   Biochim. Biophys. Acta 1209:286-292(1994).
CC   -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC       FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC       APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC       AND ALBUMIN (BY SIMILARITY).
CC   -!- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
CC       URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC       ELASTASE (BY SIMILARITY).
CC   -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC       SEPARATELY FUNCTIONING PROTEINS.
CC   -!- PTM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC       FAMILY.
CC   -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ
CC       FAMILY OF INHIBITORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D31813; BAA06600.1; -.
DR   HSSP; P10646; 1ADZ.
DR   INTERPRO; IPR000566; -.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR002345; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PFAM; PF00061; lipocalin; 1.
```

```
DR   PRINTS; PR00179; LIPOCALIN.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW   Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
KW   Lipocalin.
FT   SIGNAL       1     19       BY SIMILARITY.
FT   CHAIN       20    202       ALPHA-1 MICROGLOBULIN.
FT   CHAIN      205    346       INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
FT                               CHAIN.
FT   DOMAIN      226    281       I.
FT   DOMAIN      282    345       II.
FT   BINDING      52     52       CHROMOPHORE (BY SIMILARITY).
FT   DISULFID     90    187       BY SIMILARITY.
FT   DISULFID    230    280       BY SIMILARITY.
FT   DISULFID    239    263       BY SIMILARITY.
FT   DISULFID    255    276       BY SIMILARITY.
FT   DISULFID    286    336       BY SIMILARITY.
FT   DISULFID    295    319       BY SIMILARITY.
FT   DISULFID    311    332       BY SIMILARITY.
FT   CARBOHYD    114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    249    249       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   ACT_SITE    240    241       INHIBITORY SITE (P1) (CHYMOTRYPSIN,
FT                               ELASTASE) (BY SIMILARITY).
FT   ACT_SITE    296    297       INHIBITORY SITE (P1) (TRYPSIN) (BY
FT                               SIMILARITY).
SQ   SEQUENCE   346 AA;  38643 MW;  F1A44638109l8D5F CRC64;
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  Query Match             26.1%;  Score 247.5;  DB 1;  Length 346;
  Best Local Similarity   32.4%;  Pred. No. 5.9e-16;
  Matches   48;  Conservative   15;  Mismatches   46;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | ::   | |   | |: || |  :|: | |||| || ||:::::|||: | ||
Db     228 DSCQLTYSEGPCLGMMERYHYNGTSMACETFQYGGCLGNGNNFISEKECLQTCRTVAA-- 285

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          |    | |||||    | ||  :
Db     286 -----------------------------------CNLPIVQGPCRAYIKLWAFDAAQ 308

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     309 GKCIQFTYGGCKGNGNKFYSEKECKEYC 336
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```
RESULT   3
TFPI_RAT
ID   TFPI_RAT       STANDARD;      PRT;   302 AA.
AC   Q02445;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR (TFPI) (LIPOPROTEIN-
DE   ASSOCIATED COAGULATION INHIBITOR) (LACI) (EXTRINSIC PATHWAY INHIBITOR)
DE   (EPI).
GN   TFPI.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX   MEDLINE=92348361; PubMed=1639767;
RA   Enjyoji K.-I., Emi M., Mukai T., Kato H.;
RT   "cDNA cloning and expression of rat tissue factor pathway inhibitor
RT   (TFPI).";
RL   J. Biochem. 111:681-687(1992).
CC   -!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC       WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
CC       A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC       ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC       LIPOPROTEINS IN PLASMA.
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CC   -!- TISSUE SPECIFICITY: MOST ABUNDANT IN HEART, LUNG, KIDNEY, AND
CC       AORTIC ENDOTHELIAL CELLS.
CC   -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
CC       HIGHLY SIMILAR TO TFP2.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D10926; BAA01724.1; -.
DR   PIR; JX0213; TIRTGK.
DR   HSSP; P10646; 1TFX.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 3.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 3.
KW   Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW   Signal.
FT   SIGNAL       1     28
FT   CHAIN       29    302       TISSUE FACTOR PATHWAY INHIBITOR.
FT   DOMAIN      53    103       BPTI/KUNITZ INHIBITOR 1
FT                               (VII(A)/TISSUE FACTOR BINDING SITE).
FT   DOMAIN     124    174       BPTI/KUNITZ INHIBITOR 2
FT                               (FACTOR X(A) BINDING SITE).
FT   DOMAIN     222    272       BPTI/KUNITZ INHIBITOR 3.
FT   DISULFID    53    103       BY SIMILARITY.
FT   DISULFID    62     86       BY SIMILARITY.
FT   DISULFID    78     99       BY SIMILARITY.
FT   ACT_SITE    63     64       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID   124    174       BY SIMILARITY.
FT   DISULFID   133    157       BY SIMILARITY.
FT   DISULFID   149    170       BY SIMILARITY.
FT   ACT_SITE   134    135       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID   222    272       BY SIMILARITY.
FT   DISULFID   231    255       BY SIMILARITY.
FT   DISULFID   247    268       BY SIMILARITY.
FT   ACT_SITE   232    233       REACTIVE BOND (BY SIMILARITY).
FT   CARBOHYD   144    144       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   251    251       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   261    261       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   302 AA;  34554 MW;  F9AE82130A24A59F CRC64;
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  Query Match             26.0%;  Score 246.5;  DB 1;  Length 302;
  Best Local Similarity   34.0%;  Pred. No. 6.3e-16;
  Matches   54;  Conservative   21;  Mismatches   65;  Indels   19;  Gaps    3;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCA-TVTEN 67
           ||| : :  | ||  | |::||     |: | |||| |||||: | |||   |   | |
Db     122 DFCFLEEDPGICRGFMTRYFYNNQSKQCEQFKYGGCLGNSNNFETLEECRNTCEDPVNEV 181

Qy      68 ATGDLATSR----------NAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRA 117
             ||  |::          |      || : | :  |         :|   | :| |:|
Db     182 QKGDYVTNQITVTDRTTVNNVVIPQATKAPSQWDYDGPS--------WCLEPADSGLCKA 233

Qy     118 SFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           |  |:|::     |  | | || || |:: ::: |   |
Db     234 SEKRFYYNPAIGKCRQFNYTGCGGNNNNFTTKQDCNRAC 272
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RESULT   4
IATR_SHEEP
ID   IATR_SHEEP     STANDARD;      PRT;   123 AA.
AC   P13371;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   01-APR-1990 (Rel. 14, Last annotation update)
```

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DE   INTER-ALPHA-TRYPSIN INHIBITOR (ITI) (GIK-14) (INHIBITORY FRAGMENT OF
DE   ITI) (FRAGMENT).
OS   Ovis aries (Sheep), and Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
RN   [1]
RP   SEQUENCE.
RC   SPECIES=SHEEP;
RX   MEDLINE=87299012; PubMed=2441725;
RA   Rasp G., Hochstrasser K., Wachter E., Reisinger P.W.M.;
RT   "The amino-acid sequence of the trypsin-released inhibitor from sheep
RT   inter-alpha-trypsin inhibitor.";
RL   Biol. Chem. Hoppe-Seyler 368:727-731(1987).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=C.HIRCUS;
RX   MEDLINE=90105540; PubMed=2481505;
RA   Rasp G., Hochstrasser K., Gerl C., Wachter E.;
RT   "Primary structure of a proteinase inhibitor released from goat serum
RT   inter-alpha-trypsin inhibitor.";
RL   Biochim. Biophys. Acta 999:335-337(1989).
CC   -!- FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER
CC       LIMITED PROTEOLYSIS WITH TRYPSIN, CONTAINS TWO HOMOLOGOUS DOMAINS.
CC       WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPSIN, THE
CC       FIRST DOMAIN INTERACTS WEAKLY WITH PMN-GRANULOCYTIC ELASTASE AND
CC       NOT AT ALL WITH PANCREATIC ELASTASE.
CC   -!- MISCELLANEOUS: THE AMINO ACID AT POSITION P2' (17) APPEARS TO
CC       DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN I.
CC       INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH
CC       CHYMOTRYPSIN AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   PIR; A29652; A29652.
DR   HSSP; P10646; 1ADZ.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW   Plasma; Glycoprotein; Serine protease inhibitor; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        1     56       I.
FT   DOMAIN       57    123       II.
FT   DISULFID      5     55       BY SIMILARITY.
FT   DISULFID     14     38       BY SIMILARITY.
FT   DISULFID     30     51       BY SIMILARITY.
FT   DISULFID     61    111       BY SIMILARITY.
FT   DISULFID     70     94       BY SIMILARITY.
FT   DISULFID     86    107       BY SIMILARITY.
FT   ACT_SITE     15     16       INHIBITORY SITE (P1) (CHYMOTRYPSIN,
FT                                ELASTASE).
FT   ACT_SITE     71     72       INHIBITORY SITE (P1) (TRYPSIN).
FT   CARBOHYD     24     24       N-LINKED (GLCNAC. . .).
FT   NON_TER     123    123
SQ   SEQUENCE   123 AA;  13686 MW;  295038173F22D2D1 CRC64;
```

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  Query Match          25.8%;  Score 244.5;  DB 1;  Length 123;
  Best Local Similarity  31.8%;  Pred. No. 3.5e-16;
  Matches   47;  Conservative   15;  Mismatches   47;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |     |:::|| |  :|: | |||| || ||: :::|||: | ||
Db       3 DSCQLGYSQGPCLGMFKRYFYNGTSMACETFYYGGCMGNGNNFPSEKECLQTCRTV---- 58

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          : |    | |||||    | ||  :
Db      59 ----------------------------------QACNLPIVRGPCRAGIELWAFDAVK 83

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  |||||| || | : |:: |   |
Db      84 GKCVRFIYGGCNGNGNQFYSQKECKEYC 111
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RESULT   5
AMBP_HUMAN
ID   AMBP_HUMAN     STANDARD;      PRT;   352 AA.
AC   P02760; P02759; P00977;
DT   21-JUL-1986 (Rel. 01, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN (PROTEIN HC)
DE   (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA-
DE   TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30)].
GN   AMBP OR ITIL OR HCP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91214554; PubMed=1708673;
RA   Vetr H., Gebhard W.;
RT   "Structure of the human alpha 1-microglobulin-bikunin gene.";
RL   Biol. Chem. Hoppe-Seyler 371:1185-1196(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=87040757; PubMed=2430261;
RA   Kaumeyer J.F., Polazzi J.O., Kotick M.P.;
RT   "The mRNA for a proteinase inhibitor related to the HI-30 domain of
RT   inter-alpha-trypsin inhibitor also encodes alpha-1-microglobulin
RT   (protein HC).";
RL   Nucleic Acids Res. 14:7839-7850(1986).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=90336621; PubMed=1696200;
RA   Diarra-Mehrpour M., Bourguignon J., Sesboue R., Salier J.P.,
RA   Leveillard T., Martin J.P.;
RT   "Structural analysis of the human inter-alpha-trypsin inhibitor
RT   light-chain gene.";
RL   Eur. J. Biochem. 191:131-139(1990).
RN   [4]
RP   SEQUENCE OF 1-220 FROM N.A.
RX   MEDLINE=86312901; PubMed=2428011;
RA   Traboni C., Cortese R.;
RT   "Sequence of a full length cDNA coding for human protein HC (alpha 1
RT   microglobulin).";
RL   Nucleic Acids Res. 14:6340-6340(1986).
RN   [5]
RP   SEQUENCE OF 20-202 (INDIVIDUAL WITH TUBULAR PROTEINURIA).
RX   MEDLINE=84126849; PubMed=6198962;
RA   Lopez C., Grubb A.O., Mendez E.;
RT   "The complete amino acid sequence of human complex-forming
RT   glycoprotein heterogeneous in charge (protein HC) from one
RT   individual.";
RL   Arch. Biochem. Biophys. 228:544-554(1984).
RN   [6]
RP   SEQUENCE OF 20-198 (VARIANT).
RA   Lopez C., Grubb A.O., Mendez E.;
RT   "Human protein HC displays variability in its carboxyl-terminal amino
RT   acid sequence.";
RL   FEBS Lett. 144:349-353(1982).
RN   [7]
RP   SEQUENCE OF 20-198 (PATIENTS WITH TUBULAR PROTEINURIA).
RX   MEDLINE=81184038; PubMed=6164372;
RA   Takagi T., Takagi K., Kawai T.;
RT   "Complete amino acid sequence of human alpha 1-microglobulin.";
RL   Biochem. Biophys. Res. Commun. 98:997-1001(1981).
RN   [8]
RP   SEQUENCE OF 206-350.
RX   MEDLINE=85225968; PubMed=2408638;
RA   Reisinger P., Hochstrasser K., Albrecht G.J., Lempart K., Salier J.P.;
RT   "Human inter-alpha-trypsin inhibitor: localization of the Kunitz-type
RT   domains in the N-terminal part of the molecule and their release by
RT   trypsin-like proteinase.";
RL   Biol. Chem. Hoppe-Seyler 366:479-483(1985).
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RN   [9]
RP   CARBOHYDRATE-LINKAGE SITES.
RX   MEDLINE=82074265; PubMed=6171497;
RA   Hochstrasser K., Schoenberger O.L., Rossmanith I., Wachter E.;
RT   "Kunitz-type proteinase inhibitors derived by limited proteolysis of
RT   the inter-alpha-trypsin inhibitor, V. Attachments of carbohydrates in
RT   the human urinary trypsin inhibitor isolated by affinity
RT   chromatography.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 362:1357-1362(1981).
RN   [10]
RP   INHIBITORY SITE.
RX   MEDLINE=85225940; PubMed=3890890;
RA   Morii M., Travis J.;
RT   "The reactive site of human inter-alpha-trypsin inhibitor is in the
RT   amino-terminal half of the protein.";
RL   Biol. Chem. Hoppe-Seyler 366:19-21(1985).
RN   [11]
RP   STRUCTURE OF CARBOHYDRATES.
     MEDLINE=90306345; PubMed=1694784;
     Escribano J., Lopex-Otin C., Hjerpe A., Grubb A., Mendez E.;
     "Location and characterization of the three carbohydrate prosthetic
RT   groups of human protein HC.";
RL   FEBS Lett. 266:167-170(1990).
RN   [12]
RP   CHROMOPHORE.
RC   TISSUE=URINE;
RX   MEDLINE=91340714; PubMed=1714898;
RA   Escribano J., Grubb A., Calero M., Mendez E.;
RT   "The protein HC chromophore is linked to the cysteine residue at
RT   position 34 of the polypeptide chain by a reduction-resistant bond
RT   and causes the charge heterogeneity of protein HC.";
RL   J. Biol. Chem. 266:15758-15763(1991).
RN   [13]
RP   SEQUENCE OF 206-219, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.
RC   TISSUE=PLASMA;
RX   MEDLINE=94229087; PubMed=7513643;
RA   Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,
RA   Michalski C., Fournet B., Mizon J.;
RT   "Chondroitin sulphate covalently cross-links the three polypeptide
RT   chains of inter-alpha-trypsin inhibitor.";
RL   Eur. J. Biochem. 221:881-888(1994).
RN   [14]
RP   SEQUENCE OF 206-223, AND CROSS-LINK SITE TO HC2.
RX   MEDLINE=93232026; PubMed=7682553;
RA   Enghild J.J., Salvesen G., Thoegersen I.B., Valnickova Z.,
RA   Pizzo S.V., Hefta S.A.;
RT   "Presence of the protein-glycosaminoglycan-protein covalent cross-link
     in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain
     2/bikunin.";
RL   J. Biol. Chem. 268:8711-8716(1993).
RN   [15]
RP   SEQUENCE OF 206-223, AND CROSS-LINK SITE TO HC3.
RX   MEDLINE=91093267; PubMed=1898736;
RA   Enghild J.J., Salvesen G., Hefta S.A., Thoegersen I.B.,
RA   Rutherfurd S., Pizzo S.V.;
RT   "Chondroitin 4-sulfate covalently cross-links the chains of the human
RT   blood protein pre-alpha-inhibitor.";
RL   J. Biol. Chem. 266:747-751(1991).
RN   [16]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 230-339.
RX   MEDLINE=98227321; PubMed=9566199;
RA   Xu Y., Carr P.D., Guss J.M., Ollis D.L.;
RT   "The crystal structure of bikunin from the inter-alpha-inhibitor
RT   complex: a serine protease inhibitor with two Kunitz domains.";
RL   J. Mol. Biol. 276:955-966(1998).
CC   -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC       FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC       APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC       AND ALBUMIN.
CC   -!- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
CC       URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC       ELASTASE. ADDITIONAL PROTEOLYTIC PROCESSING IN THE KIDNEY AND/OR
CC       URINE CAN PRODUCE FURTHER AMINO- AND CARBOXYL-END MODIFICATIONS
CC       IN ITS SEQUENCE.
CC   -!- SUBUNIT: INTER-ALPHA-TRYPSIN INHIBITOR CONSIST OF A LIGHT CHAIN
CC       AND AN HEAVY CHAIN. THERE ARE THREE DIFFERENT HEAVY CHAINS.
CC   -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC       SEPARATELY FUNCTIONING PROTEINS.
CC   -!- PTM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE.
CC   -!- PTM: ADDITION OF GLYCOSAMINOGLYCAN CHONDROITIN SULFATE, ALLOWS
CC       CROSS-LINKING BETWEEN THE DIFFERENT COMPONENTS.
CC   -!- MISCELLANEOUS: IN VITRO, THE FIRST TWELVE RESIDUES OF THE AMINO
CC       END OF THE INHIBITOR APPEAR TO HAVE A REACTIVE SITE CAPABLE OF
CC       INHIBITING THE ACTIVITY OF A NUMBER OF ENZYMES. ITS IN VIVO
CC       FUNCTION IS NOT KNOWN.
CC   -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC       FAMILY.
CC   -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ
CC       FAMILY OF INHIBITORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X54816; CAA38585.1; -.
DR   EMBL; X54817; CAA38585.1; JOINED.
DR   EMBL; X54818; CAA38585.1; JOINED.
DR   EMBL; X04225; CAA27803.1; -.
DR   EMBL; M88249; AAA59196.1; -.
DR   EMBL; M88165; AAA59196.1; JOINED.
DR   EMBL; M88243; AAA59196.1; JOINED.
DR   EMBL; M88244; AAA59196.1; JOINED.
DR   EMBL; M88246; AAA59196.1; JOINED.
DR   EMBL; M88247; AAA59196.1; JOINED.
DR   EMBL; X04494; CAA28182.1; -.
DR   EMBL; X54817; CAA38586.1; -.
DR   PIR; A03217; HCHU.
DR   PIR; A25303; A25303.
DR   PIR; S13433; S13433.
DR   PIR; S10717; S10717.
DR   PDB; 1BIK; 16-MAR-99.
DR   SWISS-2DPAGE; P02760; HUMAN.
DR   MIM; 176870; -.
DR   INTERPRO; IPR000566; -.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR002345; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PFAM; PF00061; lipocalin; 1.
DR   PRINTS; PR00179; LIPOCALIN.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR   PROSITE; PS00213; LIPOCALIN; 1.
KW   Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
KW   Lipocalin; 3D-structure.

  Query Match           25.8%;  Score 244.5;  DB 1;  Length 352;
  Best Local Similarity  32.4%;  Pred. No. 1.1e-15;
  Matches   48;  Conservative   14;  Mismatches   47;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |     |::|| |  :|: | |||| || ||::|::|||: | ||
Db     229 DSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRTVAA-- 286

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          |    | |||||    | ||  :
Db     287 ------------------------------------CNLPIVRGPCRAFIQLWAFDAVK 309

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     310 GKCVLFPYGGCQGNGNKFYSEKECREYC 337
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RESULT   6
TFPI_RABIT
ID   TFPI_RABIT     STANDARD;      PRT;   300 AA.
AC   P19761; Q28828;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR (TFPI) (LIPOPROTEIN-
DE   ASSOCIATED COAGULATION INHIBITOR) (LACI) (EXTRINSIC PATHWAY INHIBITOR)
DE   (EPI).
GN   TFPI.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=91057146; PubMed=2136251;
RA   Wesselschmidt R.L., Girard T.J., Broze G.J. Jr.;
RT   "cDNA sequence of rabbit lipoprotein-associated coagulation
RT   inhibitor.";
RL   Nucleic Acids Res. 18:6440-6440(1990).
RN   [2]
RP   REVISIONS TO 72; 211 AND 218.
RC   TISSUE=LIVER;
RX   MEDLINE=92335027; PubMed=1630940;
RA   Warn-Cramer B.J., Broze G.J. Jr., Komives E.A.;
RT   "cDNA sequence of rabbit tissue factor pathway inhibitor.";
RL   Nucleic Acids Res. 20:3548-3548(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RX   MEDLINE=93276427; PubMed=8503123;
RA   Belaaouaj A., Kuppuswamy M.N., Birktoft J.J., Bajaj S.P.;
RT   "Revised cDNA sequence of rabbit tissue factor pathway inhibitor.";
RL   Thromb. Res. 69:547-553(1993).
CC   -!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC       WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
CC       A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC       ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC       LIPOPROTEINS IN PLASMA.
CC   -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
CC       HIGHLY SIMILAR TO TFP2.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X54708; CAA38515.1; ALT_SEQ.
DR   EMBL; S61902; AAB26836.1; -.
DR   PIR; S12143; S12143.
DR   HSSP; P10646; 1TFX.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 3.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 3.
KW   Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW   Signal.
FT   SIGNAL       1     24
FT   CHAIN        25    300       TISSUE FACTOR PATHWAY INHIBITOR.
FT   DOMAIN       50    100       BPTI/KUNITZ INHIBITOR 1
FT                                (VII(A)/TISSUE FACTOR BINDING SITE).
FT   DOMAIN       121   171       BPTI/KUNITZ INHIBITOR 2
FT                                (FACTOR X(A) BINDING SITE).
FT   DOMAIN       213   263       BPTI/KUNITZ INHIBITOR 3
FT                                (BY SIMILARITY).
FT   DISULFID     50    100       BY SIMILARITY.
FT   DISULFID     59    83        BY SIMILARITY.
FT   DISULFID     75    96        BY SIMILARITY.
FT   ACT_SITE     60    61        REACTIVE BOND (BY SIMILARITY).
FT   DISULFID     121   171       BY SIMILARITY.
FT   DISULFID     130   154       BY SIMILARITY.
FT   DISULFID     146   167       BY SIMILARITY.
FT   ACT_SITE     131   132       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID     213   263       BY SIMILARITY.
FT   DISULFID     222   246       BY SIMILARITY.
FT   DISULFID     238   259       BY SIMILARITY.
FT   ACT_SITE     223   224       REACTIVE BOND (BY SIMILARITY).
FT   CARBOHYD     141   141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     191   191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     252   252       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     31    31        MISSING (IN REF. 3).
FT   CONFLICT     269   272       PKSI -> RNLS (IN REF. 3).
SQ   SEQUENCE   300 AA;  34435 MW;  A08DE36537708CA6 CRC64;
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Query Match           25.7%;  Score 244;  DB 1;  Length 300;
Best Local Similarity 30.0%;  Pred. No. 1.1e-15;
Matches  48;  Conservative  23;  Mismatches  61;  Indels  28;  Gaps  2;

Qy       4 ERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCAT 63
           ::  | || ::   | ||| : |:::|:    |: |:||||:|| | : : ||| :|||
Db      43 QKPTHSFCAMKVDDGPCRAYIKRFFFNILTHQCEEFIYGGCEGNENRFESLEECKEKCAR 102

Qy      64 VTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWY 123
             |  |   :  |                                :|      | ||    |::
Db     103 DYPKMTTKLTFQKGKPD----------------------FCFLEEDPGICRGYIIRYF 135

Qy     124 FDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 163
           :: :   |  | |||| || |:: | | |   |   |||
Db     139 YNNQSKQCERFKYGGCLGNLNNFESLEECKNTC----ENP 174
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RESULT   7
AMBP_PIG
ID   AMBP_PIG       STANDARD;      PRT;   337 AA.
AC   P04366; P34954;
DT   20-MAR-1987 (Rel. 04, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN; INTER-ALPHA-
DE   TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30) (EI-14)]
DE   (FRAGMENT).
GN   AMBP OR ITIL.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90353595; PubMed=1696914;
RA   Gebhard W., Schreitmueller T., Vetr H., Wachter E., Hochstrasser K.;
RT   "Complementary DNA and deduced amino acid sequences of procine alpha
RT   1-microglobulin and bikunin.";
RL   FEBS Lett. 269:32-36(1990).
RN   [2]
RP   SEQUENCE OF 2-337 FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=91113729; PubMed=1703444;
RA   Tavakkol A.;
RT   "Molecular cloning of porcine alpha 1-microglobulin/HI-30 reveals
RT   developmental and tissue-specific expression of two variant messenger
RT   ribonucleic acids.";
RL   Biochim. Biophys. Acta 1088:47-56(1991).
RN   [3]
RP   SEQUENCE OF 212-334.
RX   MEDLINE=85225967; PubMed=2408637;
RA   Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
RT   "Kunitz-type proteinase inhibitors derived by limited proteolysis of
RT   the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
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RT   trypsin-released inhibitors from horse and pig inter-alpha-trypsin
RT   inhibitors.";
RL   Biol. Chem. Hoppe-Seyler 366:473-478(1985).
CC   -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC       FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC       APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC       AND ALBUMIN.
CC   -!- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
CC       URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC       ELASTASE.
CC   -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC       SEPARATELY FUNCTIONING PROTEINS.
CC   -!- PTM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE.
CC   -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC       FAMILY.
CC   -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ
CC       FAMILY OF INHIBITORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X53685; CAA37725.1; -.
DR   EMBL; X52087; CAA36306.1; -.
DR   PIR; A01208; TIPGBI.
DR   PIR; S11066; S11066.
DR   HSSP; P10646; 1TFX.
DR   INTERPRO; IPR000566; -.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PFAM; PF00061; lipocalin; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR   PROSITE; PS00213; LIPOCALIN; 1.
KW   Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
KW   Lipocalin.
FT   NON_TER       1      1
FT   SIGNAL       <1      4       BY SIMILARITY.
FT   CHAIN         5    188       ALPHA-1-MICROGLOBULIN.
FT   CHAIN       191    337       INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
FT                                CHAIN.
FT   DOMAIN      212    267       I.
FT   DOMAIN      268    334       II.
FT   BINDING      38     38       CHROMOPHORE (BY SIMILARITY).
FT   DISULFID     76    173       BY SIMILARITY.
FT   DISULFID    216    266
FT   DISULFID    225    249
FT   DISULFID    241    262
FT   DISULFID    272    322
FT   DISULFID    281    305
FT   DISULFID    297    318
FT   CARBOHYD    100    100       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    235    235       N-LINKED (GLCNAC. . .).
FT   ACT_SITE    226    227       INHIBITORY SITE (P1) (CHYMOTRYPSIN,
FT                                ELASTASE).
FT   ACT_SITE    282    283       INHIBITORY SITE (P1) (TRYPSIN).
FT   CONFLICT     49     49       T -> M (IN REF. 2).
FT   CONFLICT    259    259       E -> Q (IN REF. 3).
FT   CONFLICT    270    270       E -> S (IN REF. 3).
FT   CONFLICT    278    278       S -> Q (IN REF. 3).
FT   CONFLICT    283    283       G -> A (IN REF. 3).
FT   CONFLICT    285    286       FQ -> IR (IN REF. 3).
FT   CONFLICT    293    293       V -> A (IN REF. 3).
FT   CONFLICT    311    311       Q -> K (IN REF. 3).
FT   CONFLICT    315    315       E -> Q (IN REF. 3).
SQ   SEQUENCE   337 AA;  37690 MW;  1F630FF98E3CD70F CRC64;

  Query Match           25.6%;  Score 242.5;  DB 1;  Length 337;
  Best Local Similarity  31.8%;  Pred. No. 1.7e-15;
  Matches   47;  Conservative   19;  Mismatches   43;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |   : |::|| :  :|: | |||| || ||:::::|||: | ||
Db     214 DSCQLGYSQGPCLGMIKRYFYNGSSMACETFHYGGCMGNGNNFVSEKECLQTCRTV---- 269

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          | |:   |:|||  |  | ||  :
Db     270 ----------------------------------EACSLPIVSGPCRGFFQLWAFDAVQ 294

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     295 GKCVLFNYGGCQGNGNQFYSEKECKEYC 322


RESULT   8
IATR_HORSE
ID   IATR_HORSE     STANDARD;      PRT;   123 AA.
AC   P04365;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   01-APR-1990 (Rel. 14, Last annotation update)
DE   INTER-ALPHA-TRYPSIN INHIBITOR (ITI) (HI-14) (INHIBITORY FRAGMENT OF
DE   ITI) (FRAGMENT).
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=85225967; PubMed=2408637;
RA   Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
RT   "Kunitz-type proteinase inhibitors derived by limited proteolysis of
RT   the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
RT   trypsin-released inhibitors from horse and pig inter-alpha-trypsin
RT   inhibitors.";
RL   Biol. Chem. Hoppe-Seyler 366:473-478(1985).
CC   -!- FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER
CC       LIMITED PROTEOLYSIS WITH TRYPSIN, CONTAINS TWO HOMOLOGOUS DOMAINS.
CC       WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPSIN, THE
CC       FIRST DOMAIN INTERACTS WEAKLY WITH PMN-GRANULOCYTIC ELASTASE AND
CC       NOT AT ALL WITH PANCREATIC ELASTASE.
CC   -!- MISCELLANEOUS: THE AMINO ACID AT POSITION P2' (17) APPEARS TO
CC       DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN I.
CC       INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH
CC       CHYMOTRYPSIN AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   PIR; A01210; TIHOBI.
DR   HSSP; P10646; 1ADZ.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW   Plasma; Glycoprotein; Serine protease inhibitor; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        1     56       I.
FT   DOMAIN       57    123       II.
FT   DISULFID      5     55
FT   DISULFID     14     38
FT   DISULFID     30     51
FT   DISULFID     61    111
FT   DISULFID     70     94
FT   DISULFID     86    107
FT   ACT_SITE     15     16       INHIBITORY SITE (P1) (CHYMOTRYPSIN,
FT                                ELASTASE).
FT   ACT_SITE     71     72       INHIBITORY SITE (P1) (TRYPSIN).
FT   CARBOHYD     24     24       N-LINKED (GLCNAC. . .).
FT   NON_TER     123    123
SQ   SEQUENCE   123 AA;  13510 MW;  CE1A9120774411D5 CRC64;

  Query Match           25.5%;  Score 241.5;  DB 1;  Length 123;
  Best Local Similarity  31.8%;  Pred. No. 6.6e-16;
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  Matches   47;  Conservative   15;  Mismatches   47;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |   : |::|| |  :|: | |||| || ||: :::|||: | ||
Db       3 DSCQLDHAQGPCLGMISRYFYNGTSMACETFQYGGCLGNGNNFASQKECLQTCRTVAA-- 60

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                |    | |||||    | ||  :
Db      61 -----------------------------------CNLPIVQGPCRAFIRLWAFDAAQ 83

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | |||||||  | : |:: |   |
Db      84 GKCVLFTYGGCRGNGNKFYSQKECKEYC 111


RESULT   9
AMBP_RAT
ID   AMBP_RAT       STANDARD;      PRT;   349 AA.
AC   Q64240; Q63336;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN; INTER-ALPHA-
DE   TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30)].
GN   AMBP OR ITIL.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=92182014; PubMed=1371936;
RA   Lindqvist A., Bratt T., Altieri M., Kastern W., Aakerstroem B.;
RT   "Rat alpha 1-microglobulin: co-expression in liver with the light
RT   chain of inter-alpha-trypsin inhibitor.";
RL   Biochim. Biophys. Acta 1130:63-67(1992).
RN   [2]
RP   SEQUENCE OF 141-195 FROM N.A.
RX   MEDLINE=87033744; PubMed=2429963;
RA   Kastern W., Bjoerck L., Aakerstroem B.;
RT   "Developmental and tissue-specific expression of alpha 1-microglobulin
RT   mRNA in the rat.";
RL   J. Biol. Chem. 261:15070-15074(1986).
CC   -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC       FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC       APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC       AND ALBUMIN (BY SIMILARITY).
CC   -!- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
CC       URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC       ELASTASE (BY SIMILARITY).
CC   -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC       SEPARATELY FUNCTIONING PROTEINS.
CC   -!- PTM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC       FAMILY.
CC   -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ
CC       FAMILY OF INHIBITORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S87544; AAB21782.1; -.
DR   EMBL; J02600; AAA41596.1; -.
DR   HSSP; P12111; 1KUN.
DR   INTERPRO; IPR000566; -.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR002345; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PFAM; PF00061; lipocalin; 1.
DR   PRINTS; PR00179; LIPOCALIN.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR   PROSITE; PS00213; LIPOCALIN; 1.
KW   Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
KW   Lipocalin.
FT   SIGNAL       1     19       BY SIMILARITY.
FT   CHAIN       20    202       ALPHA-1-MICROGLOBULIN.
FT   CHAIN      205    349       INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
FT                               CHAIN.
FT   DOMAIN      226    281       I.
FT   DOMAIN      282    348       II.
FT   BINDING      52     52       CHROMOPHORE (BY SIMILARITY).
FT   DISULFID     90    187       BY SIMILARITY.
FT   DISULFID    230    280       BY SIMILARITY.
FT   DISULFID    239    263       BY SIMILARITY.
FT   DISULFID    255    276       BY SIMILARITY.
FT   DISULFID    286    336       BY SIMILARITY.
FT   DISULFID    295    319       BY SIMILARITY.
FT   DISULFID    311    332       BY SIMILARITY.
FT   CARBOHYD    114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    233    233       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   ACT_SITE    240    241       INHIBITORY SITE (P1) (CHYMOTRYPSIN,
FT                               ELASTASE) (BY SIMILARITY).
FT   ACT_SITE    296    297       INHIBITORY SITE (P1) (TRYPSIN) (BY
FT                               SIMILARITY).
FT   CONFLICT    142    142       G -> A (IN REF. 2).
SQ   SEQUENCE   349 AA;  38851 MW;  1B7FB7DCB0824E01 CRC64;


  Query Match             25.1%;  Score 237.5;  DB 1;  Length 349;
  Best Local Similarity   30.4%;  Pred. No. 5.1e-15;
  Matches   45;  Conservative   17;  Mismatches   47;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | ::   | |     :::||    :|: | |||| || ||: :::|||: | |:
Db     228 DSCQLNYSEGPCLGMQQKYYYNGASMACETFQYGGCLGNGNNFASEKECLQTCRTIAA-- 285

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                |    | |||||    | ||  :
Db     286 -----------------------------------CNLPIVQGPCRAFAELWAFDAAQ 308

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  ||||||:|| | : ||: |   |
Db     309 GKCIQFIYGGCKGNGNKFYSEKECKEYC 336


RESULT  10
TFPI_MACMU
ID   TFPI_MACMU     STANDARD;      PRT;   304 AA.
AC   Q28864;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR (TFPI) (LIPOPROTEIN-
DE   ASSOCIATED COAGULATION INHIBITOR) (LACI) (EXTRINSIC PATHWAY INHIBITOR)
DE   (EPI).
GN   TFPI1 OR TFPI.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=94375417; PubMed=8089087;
RA   Kamei S., Kamikubo Y., Hamuro T., Fujimoto H., Ishihara M.,
RA   Yonemura H., Miyamoto S., Funatsu A., Enjyoji K., Abumiya T.;
RT   "Amino acid sequence and inhibitory activity of rhesus monkey tissue
RT   factor pathway inhibitor (TFPI): comparison with human TFPI.";
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RL   J. Biochem. 115:708-714(1994).
CC   -!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC       WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
CC       A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC       ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC       LIPOPROTEINS IN PLASMA.
CC   -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC   -!- PTM: O-GLYCOSYLATED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
CC       HIGHLY SIMILAR TO TFP2.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S73337; AAB31955.1; -.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 3.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 3.
KW   Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW   Signal.
FT   SIGNAL       1     28       BY SIMILARITY.
FT   CHAIN       29    304       TISSUE FACTOR PATHWAY INHIBITOR.
FT   DOMAIN      54    104       BPTI/KUNITZ INHIBITOR 1
FT                               (VII(A)/TISSUE FACTOR BINDING SITE).
FT   DOMAIN     125    175       BPTI/KUNITZ INHIBITOR 2
FT                               (FACTOR X(A) BINDING SITE).
FT   DOMAIN     217    267       BPTI/KUNITZ INHIBITOR 3.
FT   DISULFID    54    104       BY SIMILARITY.
FT   DISULFID    63     87       BY SIMILARITY.
FT   DISULFID    79    100       BY SIMILARITY.
FT   ACT_SITE    64     65       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID   125    175       BY SIMILARITY.
FT   DISULFID   134    158       BY SIMILARITY.
FT   DISULFID   150    171       BY SIMILARITY.
FT   ACT_SITE   135    136       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID   217    267       BY SIMILARITY.
FT   DISULFID   226    250       BY SIMILARITY.
FT   DISULFID   242    263       BY SIMILARITY.
FT   ACT_SITE   227    228       REACTIVE BOND (BY SIMILARITY).
FT   CARBOHYD   145    145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   256    256       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   304 AA;  35085 MW;  56E13B3FF16282B0 CRC64;
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  Query Match             24.9%;  Score 236.5;  DB 1;  Length 304;
  Best Local Similarity   34.9%;  Pred. No. 5.4e-15;
  Matches   53;  Conservative   24;  Mismatches   64;  Indels   11;  Gaps    4;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           |||  :  :  | ||  : |::||     |: | |||| || ||: | |||   |    :
Db     123 DFCFLEEDPGICRGYITRYFYNNQSKQCERFKYGGCLGNMNNFETLEECKNTC---EDGL 179

Qy      69 TG----DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124
             |    :  |  || ::|    |  | ::  |   |:   :| | |  | |||:  |:|:
Db     180 NGFQVDNYGTQLNAVNNS--QTP--QSTKVPSFFEFHGPSWCLAPADRGLCRANENRFYY 235

Qy     125 DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           :     |  | | || ||:|:: |:  |:  |
Db     236 NSVIGKCRPFKYSGCGGNENNFTSKRECLRAC 267
```

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RESULT  11
AMBP_MESAU
ID   AMBP_MESAU     STANDARD;      PRT;   349 AA.
AC   Q60559; Q60558;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN; INTER-ALPHA-
DE   TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30)].
GN   AMBP OR ITIL.
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=95110820; PubMed=7529051;
RA   Ide H., Itoh H., Nawa Y.;
RT   "Sequencing of cDNAs encoding alpha 1-microglobulin/bikunin of
RT   Mongolian gerbil and Syrian golden hamster in comparison with man and
RT   other species.";
RL   Biochim. Biophys. Acta 1209:286-292(1994).
CC   -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC       FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC       APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC       AND ALBUMIN (BY SIMILARITY).
CC   -!- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
CC       URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC       ELASTASE (BY SIMILARITY).
CC   -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC       SEPARATELY FUNCTIONING PROTEINS.
CC   -!- PTM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC       FAMILY.
CC   -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ
CC       FAMILY OF INHIBITORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D31814; BAA06601.1; -.
DR   HSSP; P10646; 1TFX.
DR   INTERPRO; IPR000566; -.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR002345; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PFAM; PF00061; lipocalin; 1.
DR   PRINTS; PR00179; LIPOCALIN.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR   PROSITE; PS00213; LIPOCALIN; 1.
KW   Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
KW   Lipocalin.
FT   SIGNAL       1     19       BY SIMILARITY.
FT   CHAIN       20    202       ALPHA-1-MICROGLOBULIN.
FT   CHAIN      205    349       INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
FT                               CHAIN.
FT   DOMAIN     226    281       I.
FT   DOMAIN     282    348       II.
FT   BINDING     52     52       CHROMOPHORE (BY SIMILARITY).
FT   DISULFID    90    187       BY SIMILARITY.
FT   DISULFID   230    280       BY SIMILARITY.
FT   DISULFID   239    263       BY SIMILARITY.
FT   DISULFID   255    276       BY SIMILARITY.
FT   DISULFID   286    336       BY SIMILARITY.
FT   DISULFID   295    319       BY SIMILARITY.
FT   DISULFID   311    332       BY SIMILARITY.
FT   CARBOHYD    35     35       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT   ACT_SITE    240    241       INHIBITORY SITE (P1) (CHYMOTRYPSIN,
FT                                ELASTASE) (BY SIMILARITY).
FT   ACT_SITE    296    297       INHIBITORY SITE (P1) (TRYPSIN) (BY
FT                                SIMILARITY).
SQ   SEQUENCE   349 AA;  38782 MW;  8C954584B7DBE728 CRC64;


  Query Match             24.8%;  Score 235.5;  DB 1;  Length 349;
  Best Local Similarity   31.1%;  Pred. No. 7.8e-15;
  Matches   46;  Conservative   17;  Mismatches   46;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :|   | |   : :::||    :|: | |||| || ||: :::|||: | ||
Db     228 DSCQLSYSEGPCLGMIEKYYYNGASMACETFHYGGCLGNGNNFNSEKECLQTCRTVAA-- 285

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                |:   | |||||    | ||  :
Db     286 -----------------------------------CSLPIVQGPCRAYVELWAFDAAQ 308

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     309 GKCVQFSYGGCKGNGNKFYSEKECKEYC 336


RESULT  12
AMBP_MOUSE
ID   AMBP_MOUSE     STANDARD;      PRT;   349 AA.
AC   Q07456; Q61294;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1-MICROGLOBULIN; INTER-ALPHA-
DE   TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI-30)].
GN   AMBP OR ITIL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=LIVER;
RX   MEDLINE=93363639; PubMed=7689339;
RA   Chan P., Salier J.P.;
RT   "Mouse alpha-1-microglobulin/bikunin precursor: cDNA analysis, gene
RT   evolution and physical assignment of the gene next to the orosomucoid
RT   locus.";
RL   Biochim. Biophys. Acta 1174:195-200(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=LIVER;
RX   MEDLINE=95189774; PubMed=7533761;
RA   Itoh H., Ide H., Kataoka H., Tomita M., Yoshihara H., Nawa Y.;
RT   "cDNA sequencing of mouse alpha 1-microglobulin/inter-alpha-trypsin
RT   inhibitor light chain and its expression in acute inflammation.";
RL   J. Biochem. 116:767-772(1994).
RN   [3]
RP   SEQUENCE OF 128-349 FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=LIVER;
RA   Itoh H., Ide H., Yoshihara H., Nawa Y.;
RL   Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC       FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC       APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC       AND ALBUMIN (BY SIMILARITY).
CC   -!- FUNCTION: INTER-ALPHA-TRYPSIN INHIBITOR, PRESENT IN PLASMA AND
CC       URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC       ELASTASE (BY SIMILARITY).
CC   -!- SUBUNIT: INTER-ALPHA-TRYPSIN INHIBITOR CONSIST OF A LIGHT CHAIN
CC       AND AN HEAVY CHAIN. THERE ARE THREE DIFFERENT HEAVY CHAINS.
CC   -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC       SEPARATELY FUNCTIONING PROTEINS.
CC   -!- PTM: HC CONTAINS A COVALENTLY LINKED BROWN-YELLOW CHROMOPHORE (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC       FAMILY.
CC   -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE BPTI/KUNITZ
CC       FAMILY OF INHIBITORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X68680; CAA48640.1; -.
DR   EMBL; D28812; BAA05973.1; -.
DR   HSSP; P12111; 1KUN.
DR   MGD; MGI:88002; AMBP.
DR   INTERPRO; IPR000566; -.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR002345; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PFAM; PF00061; lipocalin; 1.
DR   PRINTS; PR00179; LIPOCALIN.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR   PROSITE; PS00213; LIPOCALIN; 1.
KW   Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
KW   Lipocalin.
FT   SIGNAL       1     19       BY SIMILARITY.
FT   CHAIN       20    202       ALPHA-1-MICROGLOBULIN.
FT   CHAIN      205    349       INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
FT                               CHAIN.
FT   DOMAIN      226    281       I.
FT   DOMAIN      282    348       II.
FT   BINDING      52     52       CHROMOPHORE (BY SIMILARITY).
FT   DISULFID     90    187       BY SIMILARITY.
FT   DISULFID    230    280       BY SIMILARITY.
FT   DISULFID    239    263       BY SIMILARITY.
FT   DISULFID    255    276       BY SIMILARITY.
FT   DISULFID    286    336       BY SIMILARITY.
FT   DISULFID    295    319       BY SIMILARITY.
FT   DISULFID    311    332       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    233    233       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   ACT_SITE    240    241       INHIBITORY SITE (P1) (CHYMOTRYPSIN,
FT                               ELASTASE) (BY SIMILARITY).
FT   ACT_SITE    296    297       INHIBITORY SITE (P1) (TRYPSIN) (BY
FT                               SIMILARITY).
FT   CONFLICT     65     65       Q -> S (IN REF. 2).
SQ   SEQUENCE   349 AA;  39070 MW;  CE4D9FC7375DA80B CRC64;


  Query Match             24.8%;  Score 235.5;  DB 1;  Length 349;
  Best Local Similarity   29.7%;  Pred. No. 7.8e-15;
  Matches   44;  Conservative   18;  Mismatches   47;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | ::   | |     |::||    :|: | |||| || ||:::::::||: | |:
Db     228 DSCQLNYSEGPCLGMQERYYYNGASMACETFQYGGCLGNGNNFISEKDCLQTCRTIAA-- 285

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                              |    | |||||    | ||  :
Db     286 -----------------------------------CNLPIVQGPCRAFIKLWAFDAAQ 308

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     309 GKCIQFHYGGCKGNGNKFYSEKECKEYC 336


RESULT  13
TFPI_HUMAN
ID   TFPI_HUMAN     STANDARD;      PRT;   304 AA.
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AC   P10646;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR (TFPI) (LIPOPROTEIN-
DE   ASSOCIATED COAGULATION INHIBITOR) (LACI) (EXTRINSIC PATHWAY INHIBITOR)
DE   (EPI).
GN   TFPI1 OR TFPI OR LACI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88198127; PubMed=2452157;
RA   Wun T.-C., Kretzmer K.K., Girard T.J., Miletich J.P., Broze G.J. Jr.;
RT   "Cloning and characterization of a cDNA coding for the lipoprotein-
RT   associated coagulation inhibitor shows that it consists of three
RT   tandem Kunitz-type inhibitory domains.";
RL   J. Biol. Chem. 263:6001-6004(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91129227; PubMed=1993173;
RA   van der Logt C.P.E., Reitsma P.H., Bertina R.M.;
RT   "Intron-exon organization of the human gene coding for the
RT   lipoprotein-associated coagulation inhibitor: the factor Xa dependent
RT   inhibitor of the extrinsic pathway of coagulation.";
RL   Biochemistry 30:1571-1577(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91161593; PubMed=2002045;
RA   Girard T.J., Eddy R., Wesselschmidt R.L., Macphail L.A.,
RA   Likert K.M., Byers M.G., Shows T.B., Broze G.J. Jr.;
RT   "Structure of the human lipoprotein-associated coagulation inhibitor
RT   gene. Intro/exon gene organization and localization of the gene to
RT   chromosome 2.";
RL   J. Biol. Chem. 266:5036-5041(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89388722; PubMed=2781520;
RA   Girard T.J., Warren L.A., Novotny W.F., Bejcek B.E., Miletich J.P.,
RA   Broze G.J. Jr.;
RT   "Identification of the 1.4 kb and 4.0 kb messages for the lipoprotein
RT   associated coagulation inhibitor and expression of the encoded
RT   protein.";
RL   Thromb. Res. 55:37-50(1989).
RN   [5]
RP   SEQUENCE OF 29-50.
RX   MEDLINE=90036996; PubMed=2553722;
RA   Novotny W.F., Girard T.J., Miletich J.P., Broze G.J. Jr.;
RT   "Purification and characterization of the lipoprotein-associated
RT   coagulation inhibitor from human plasma.";
RL   J. Biol. Chem. 264:18832-18837(1989).
RN   [6]
RP   INHIBITORY SITES.
RX   MEDLINE=89181950; PubMed=2927510;
RA   Girard T.J., Warren L.A., Novotny W.F., Likert K.M., Brown S.G.,
RA   Miletich J.P., Broze G.J. Jr.;
RT   "Functional significance of the Kunitz-type inhibitory domains of
RT   lipoprotein-associated coagulation inhibitor.";
RL   Nature 338:518-520(1989).
RN   [7]
RP   CARBOHYDRATE-LINKAGE SITES.
RX   MEDLINE=96224851; PubMed=8639592;
RA   Nakahara Y., Miyata T., Hamuro T., Funatsu A., Miyagi M.,
RA   Tsunasawa S., Kato H.;
RT   "Amino acid sequence and carbohydrate structure of a recombinant
RT   human tissue factor pathway inhibitor expressed in Chinese hamster
RT   ovary cells: one N-and two O-linked carbohydrate chains are located
RT   between Kunitz domains 2 and 3 and one N-linked carbohydrate chain is
RT   in Kunitz domain 2.";
RL   Biochemistry 35:6450-6459(1996).
RN   [8]
RP   REVIEW.
RX   MEDLINE=91104709; PubMed=2271516;
RA   Broze G.J. Jr., Girard T.J., Novotny W.F.;
RT   "Regulation of coagulation by a multivalent Kunitz-type inhibitor.";
RL   Biochemistry 29:7539-7546(1990).
RN   [9]
RP   STRUCTURE BY NMR OF 121-182.
RX   MEDLINE=97342711; PubMed=9199408;
RA   Burgering M.J., Orbons L.P., van der Doelen A., Mulders J.,
RA   Theunissen H.J., Grootenhuis P.D., Bode W., Huber R., Stubbs M.T.;
RT   "The second Kunitz domain of human tissue factor pathway inhibitor:
RT   cloning, structure determination and interaction with factor Xa.";
RL   J. Mol. Biol. 269:395-407(1997).
CC   -!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC       WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
CC       A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC       ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC       LIPOPROTEINS IN PLASMA.
CC   -!- TISSUE SPECIFICITY: MOSTLY IN ENDOTHELIAL CELLS.
CC   -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC   -!- PTM: O-GLYCOSYLATED.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
CC       HIGHLY SIMILAR TO TFP2.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J03225; AAA52022.1; -.
DR   EMBL; M58650; AAA59480.1; -.
DR   EMBL; M58644; AAA59480.1; JOINED.
DR   EMBL; M58645; AAA59480.1; JOINED.
DR   EMBL; M58646; AAA59480.1; JOINED.
DR   EMBL; M58647; AAA59480.1; JOINED.
DR   EMBL; M58648; AAA59480.1; JOINED.
DR   EMBL; M58649; AAA59480.1; JOINED.
DR   EMBL; M59499; AAA59526.1; -.
DR   EMBL; M59493; AAA59526.1; JOINED.
DR   EMBL; M59494; AAA59526.1; JOINED.
DR   EMBL; M59495; AAA59526.1; JOINED.
DR   EMBL; M59496; AAA59526.1; JOINED.
DR   EMBL; M59497; AAA59526.1; JOINED.
DR   EMBL; M59498; AAA59526.1; JOINED.
DR   PIR; A28650; TIHUGK.
DR   PIR; A34315; A34315.
DR   PIR; A60433; A60433.
DR   PIR; S03903; S03903.
DR   PDB; 1ADZ; 25-FEB-98.
DR   PDB; 1TFX; 21-JAN-98.
DR   MIM; 152310; -.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 3.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 3.
KW   Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW   Signal; 3D-structure.
FT   SIGNAL       1     28
FT   CHAIN       29    304       TISSUE FACTOR PATHWAY INHIBITOR.
FT   DOMAIN      54    104       BPTI/KUNITZ INHIBITOR 1
FT                               (VII(A)/TISSUE FACTOR BINDING SITE).
FT   DOMAIN     125    175       BPTI/KUNITZ INHIBITOR 2
FT                               (FACTOR X(A) BINDING SITE).
FT   DOMAIN     217    267       BPTI/KUNITZ INHIBITOR 3.
FT   DISULFID    54    104       BY SIMILARITY.
FT   DISULFID    63     87       BY SIMILARITY.
FT   DISULFID    79    100       BY SIMILARITY.
FT   ACT_SITE    64     65       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID   125    175       BY SIMILARITY.
FT   DISULFID   134    158       BY SIMILARITY.
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FT   DISULFID    150     171       BY SIMILARITY.
FT   ACT_SITE    135     136       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    217     267       BY SIMILARITY.
FT   DISULFID    226     250       BY SIMILARITY.
FT   DISULFID    242     263       BY SIMILARITY.
FT   ACT_SITE    227     228       REACTIVE BOND (BY SIMILARITY).
FT   CARBOHYD    145     145       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    202     202
FT   CARBOHYD    203     203
FT   CARBOHYD    195     195       N-LINKED (GLCNAC. . .).
FT   MUTAGEN      64      64       K->I: ABOLISHES INHIBITION OF VII(A)/TF.
FT   MUTAGEN     135     135       R->L: ABOLISHES INHIBITION OF X(A).
FT   MUTAGEN     227     227       R->L: ABOLISHES INHIBITION OF VII(A)/TF.
SQ   SEQUENCE   304 AA;  35015 MW;  5281E32B758B44FE CRC64;

  Query Match           24.6%;  Score 233.5;  DB 1;  Length 304;
  Best Local Similarity  33.6%;  Pred. No. 1e-14;
  Matches   51;  Conservative   26;  Mismatches   64;  Indels   11;  Gaps    3;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           |||  :  :  | ||  : |::||     |: | |||| || ||: | |||   |    :
Db     123 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC---EDGP 179

Qy      69 TG----DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124
             |    :  |  || ::|:      | ::  |   |:   :|   |  | |||:  |:|:
Db     180 NGFQVDNYGTQLNAVNNSLTP----QSTKVPSLFEFHGPSWCLTPADRGLCRANENRFYY 235

Qy     125 DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           :    |  | | || ||:|:: |:: |:  |
Db     236 NSVIGKCRPFKYSGCGGNENNFTSKQECLRAC 267

RESULT  14
TFP2_HUMAN
ID   TFP2_HUMAN     STANDARD;      PRT;   235 AA.
AC   P48307;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR (TFPI-2) (PLACENTAL
DE   PROTEIN 5) (PP5).
GN   TFPI2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=PLACENTA;
RX   MEDLINE=95204397; PubMed=7896752;
RA   Miyagi Y., Koshikawa N., Yasumitsu H., Miyagi E., Hirahara F.,
RA   Aoki I., Misugi K., Umeda M., Miyazaki K.;
RT   "cDNA cloning and mRNA expression of a serine proteinase inhibitor
RT   secreted by cancer cells: identification as placental protein 5 and
RT   tissue factor pathway inhibitor-2.";
RL   J. Biochem. 116:939-942(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE=94211862; PubMed=8159751;
RA   Sprecher C.A., Kisiel W., Mathewes S., Foster D.C.;
RT   "Molecular cloning, expression, and partial characterization of a
RT   second human tissue-factor-pathway inhibitor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:3353-3357(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Maggi L.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   PARTIAL SEQUENCE OF 23-35; 47-53 AND 133-146.
RC   TISSUE=PLACENTA;
RX   MEDLINE=88106628; PubMed=3276312;
RA   Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaelae M.;
RT   "Purification and characterization of placental protein 5.";
RL   Biochem. Biophys. Res. Commun. 150:483-490(1988).
RN   [5]
RP   ERRATUM.
RA   Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaelae M.;
RL   Biochem. Biophys. Res. Commun. 151:630-631(1988).
CC   -!- FUNCTION: SEEMS TO INHIBIT TRYPSIN, FACTOR VII(A)/TISSUE FACTOR,
CC       WEAKLY FACTOR XA. HAS NO EFFECT ON THROMBIN.
CC   -!- TISSUE SPECIFICITY: UMBILICAL VEIN ENDOTHELIAL CELLS, LIVER,
CC       PLACENTA, HEART, PANCREAS, AND MATERNAL SERUM AT ADVANCED
CC       PREGNANCY.
CC   -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
CC       HIGHLY SIMILAR TO TPFI.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D29992; BAA06272.1; -.
DR   EMBL; L27624; AAA20094.1; -.
DR   EMBL; AC002076; AAB54049.1; -.
DR   PIR; A34029; A34029.
DR   PIR; B34029; B34029.
DR   PIR; C34029; C34029.
DR   HSSP; P12111; 1KNT.
DR   MIM; 600033; -.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 3.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 3.
KW   Serine protease inhibitor; Glycoprotein; Repeat; Signal;
KW   Blood coagulation.
FT   SIGNAL        1     22
FT   CHAIN        23    235       TISSUE FACTOR PATHWAY INHIBITOR 2.
FT   DOMAIN       36     86       BPTI/KUNITZ INHIBITOR 1.
FT   DOMAIN       96    149       BPTI/KUNITZ INHIBITOR 2.
FT   DOMAIN      158    208       BPTI/KUNITZ INHIBITOR 3.
FT   DOMAIN      213    217       POLY-LYS.
FT   ACT_SITE     46     47       REACTIVE BOND (BY SIMILARITY).
FT   ACT_SITE    107    108       REACTIVE BOND (BY SIMILARITY).
FT   ACT_SITE    168    169       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID     36     86       BY SIMILARITY.
FT   DISULFID     45     69       BY SIMILARITY.
FT   DISULFID     61     82       BY SIMILARITY.
FT   DISULFID     96    149       BY SIMILARITY.
FT   DISULFID    106    130       BY SIMILARITY.
FT   DISULFID    122    145       BY SIMILARITY.
FT   DISULFID    158    208       BY SIMILARITY.
FT   DISULFID    167    191       BY SIMILARITY.
FT   DISULFID    183    204       BY SIMILARITY.
FT   CARBOHYD    116    116       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     23     23       D -> A (IN REF. 4).
SQ   SEQUENCE   235 AA;  26934 MW;  975ABA5C53F7C65F CRC64;

  Query Match           22.6%;  Score 214.5;  DB 1;  Length 235;
  Best Local Similarity  25.9%;  Pred. No. 4.4e-13;
  Matches   53;  Conservative   31;  Mismatches   66;  Indels   55;  Gaps    5;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC------- 61
             : ||:    | ||| : |::|:    ||: |:||||:||:||: | | |   |
Db      34 EICLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDDACWRIEKVP 93

Qy      62 ------ATVTENATGDL----------------ATSRNAADSSVPS--------APRR 88
                :| :  |                      ||  ::  |         ||::
Db      94 KVCRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCAPKK 153
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Qy      90 QDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSE 149
           |            :| :    | | |:  |:||:    :|: | | || || |:: |
Db     154 IPS-----------FCYSPKDEGLCSANVTRYYFNPRYRTCDAFTYTGCGGNDNNFVSR 201

Qy     150 EACMLRCF----RQQENPPLPLGSK 170
           | |   |     :::: | |   |:
Db     202 EDCKRACAKALKKKKKMPKLRFASR 226
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RESULT  15
APP2_RAT
ID   APP2_RAT       STANDARD;      PRT;   765 AA.
AC   P15943;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   AMYLOID-LIKE PROTEIN 2 PRECURSOR (SPERM MEMBRANE PROTEIN YWK-II).
GN   APLP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE OF 1-627 FROM N.A.
RC   STRAIN=WISTAR; TISSUE=BRAIN, AND HEART;
RX   MEDLINE=94368849; PubMed=8086458;
RA   Sandbrink R., Masters C.L., Beyreuther K.;
RT   "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT   protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RT   difference to human and murine homologues.";
RL   Biochim. Biophys. Acta 1219:167-170(1994).
RN   [2]
RP   SEQUENCE OF 575-765 FROM N.A.
RC   TISSUE=TESTIS;
RX   MEDLINE=90207205; PubMed=1690887;
RA   Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
RT   "Characterization of cDNA encoding a human sperm membrane protein
RT   related to A4 amyloid protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), B, C AND D;
CC       ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: CONTAINS A PROTEASE INHIBITOR DOMAIN BELONGING TO
CC       THE BPTI/KUNITZ FAMILY OF INHIBITORS.
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X77934; CAA54906.1; -.
DR   EMBL; M31322; AAA42352.1; -.
DR   PIR; A35981; A35981.
DR   HSSP; P05067; 1CA0.
DR   INTERPRO; IPR001868; -.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Transmembrane; Alternative splicing; Serine protease inhibitor;
KW   Signal; Glycoprotein.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    765       AMYLOID-LIKE PROTEIN 2.
FT   DOMAIN       30    695       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    696    718       POTENTIAL.
FT   DOMAIN      719    765       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      218    282       ASP/GLU-RICH (HIGHLY ACIDIC).
FT   DOMAIN      308    366       BPTI/KUNITZ INHIBITOR.
FT   ACT_SITE    322    323       REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    312    362       BY SIMILARITY.
FT   DISULFID    321    345       BY SIMILARITY.
FT   DISULFID    337    358       BY SIMILARITY.
FT   DOMAIN      218    229       POLY-GLU.
FT   CARBOHYD    628    628       O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT   VARSPLIC    311    365       MISSING (IN ISOFORM C AND ISOFORM D).
FT   VARSPLIC    616    627       MISSING (IN ISOFORM B AND ISOFORM D).
FT   CONFLICT    575    577       DQF -> EFV (IN REF. 2).
SQ   SEQUENCE   765 AA;  86882 MW;  CF51FCCCE305A0CF CRC64;
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  Query Match             22.2%;  Score 210;  DB 1;  Length 765;
  Best Local Similarity   27.5%;  Pred. No. 4.3e-12;
  Matches   58;  Conservative   22;  Mismatches   55;  Indels   76;  Gaps    3;

Qy      28 WYNVTDGSC-----QLFVYG-----GCDG--------------NSNNYLTKEE------ 58
           |: |   :|      |: ||     | |                :|:: ::|||
Db     166 WHTVVKEACLTEGMTLYSYGMLLPCGVDQFHGTEYVCCPQTKVVDSDSTMSKEEEEPEEE 225

Qy      57 ------CLKKCATVTENATGDLATSRNAADSSVPSAPRRQDSE--------DHSSDMFNY 102
                | |    ||    ||     ||          :: |         |:  | |
Db     226 DEEEDYALDKSEFPTE---ADLEDFTEAAADEDEDEEEEEEEEGEEVVEDRDYYYDSFKG 282

Qy     103 EEY-------------------------CTANAVTGPCRASFPRWYFDVERNSCNNFIY 136
           ::|                         |:  |:||||||  ||||||: :  |  |||
Db     283 DDYNEENPTEPSSDGTISDKEIAHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIY 342

Qy     137 GGCRGNKNSYRSEEACMLRCFRQQENPPLPL 167
           ||| ||:|:: ||: || |  :   || ||
Db     343 GGCGGNRNNFESEDYCMAVC--KTMIPPTPL 371
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Search completed: January 31, 2001, 15:05:07
Job time: 119 sec
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RESULT   5
Q9WU04
ID   Q9WU04      PRELIMINARY;      PRT;   195 AA.
AC   Q9WU04;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2 SPLICE VARIANT 1.
GN   HAI2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
     STRAIN=BALB/C;
     MEDLINE=99160423; PubMed=10049781;
     Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
RT   "Hepatocyte growth factor activator inhibitor type 2 lacking the first
RT   Kunitz-type serine proteinase inhibitor domain is a predominant
RT   product in mouse but not in human.";
RL   Biochem. Biophys. Res. Commun. 255:740-748(1999).
DR   EMBL; AF099019; AAD22173.1; -.
DR   HSSP; P05067; 1TAW.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 1.
KW   Serine protease inhibitor.
SQ   SEQUENCE   195 AA;  21736 MW;  EF49C83AB4E3EDE0 CRC64;

  Query Match           40.2%;  Score 381;  DB 11;  Length 195;
  Best Local Similarity  64.5%;  Pred. No. 1.7e-33;
  Matches   69;  Conservative   14;  Mismatches   24;  Indels    0;  Gaps    0;

Qy      64 VTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWY 123
           | || | |:| :|| ||||| | ||:| :|| |:::|||||||   ||||||||:|||||
Db      34 VHENTTDDMARNRNGADSSVLSVPRKQSAEDLSAEIFNYEEYCVPKAVTGPCRAAFPRWY 93

Qy     124 FDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           :| |:||| :|||||||||||||| |:|||| |  :| :| |  | |
Db      94 YDTEKNSCISFIYGGCRGNKNSYLSQEACMQHCSGKQMHPFLTPGLK 140


RESULT   6
O43278
ID   O43278      PRELIMINARY;      PRT;   513 AA.
AC   O43278;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97197808; PubMed=9045658;
RA   Shimomura T., Denda K., Kitamura A., Kawaguchi T., Kito M., Kondo J.,
RA   Kagaya S., Qin L., Takata H., Miyazawa K., Kitamura N.;
RT   "Hepatocyte growth factor activator inhibitor, a novel Kunitz-type
RT   serine protease inhibitor.";
RL   J. Biol. Chem. 272:6370-6376(1997).
DR   EMBL; AB000095; BAA25014.1; -.
DR   HSSP; P31713; 1SHP.
DR   INTERPRO; IPR002172; -.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PFAM; PF00057; ldl_recept_a; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 2.
DR   PROSITE; PS01209; LDLRA_1; 1.
DR   PROSITE; PS50068; LDLRA_2; 1.
KW   Glycoprotein; Serine protease inhibitor.
SQ   SEQUENCE   513 AA;  56885 MW;  D6E05F3A5885CDDD CRC64;

  Query Match           32.9%;  Score 312;  DB 4;  Length 513;
  Best Local Similarity  33.5%;  Pred. No. 1.4e-25;
  Matches   67;  Conservative   24;  Mismatches   71;  Indels   38;  Gaps

Qy       5 RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATV 64
           :  |:|| |  ||||| | |||:|: |:  |: |||||| || |||| :|||:  |  !
Db     244 KQTEDYCLASNKVGRCRGSFPRWYYDPTEQICKSFVYGGCLGNKNNYLREEECILACRGV 303

Qy      65 --------------TENATGDLATSRNAADS-----SVPSAPRRQDS---EDHSSDMFNY 102
                         |  |    ::    ||       |: |   |    | ::|
Db     304 QGPSMERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDEL 363

Qy     103 EE--------YCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACML 154
           :         :|     || |: | ||||::     |  | |||| ||||::  |: |:
Db     364 QRIHFPSDKGHCVDLPDTGLCKESIPRWYYNPFSEHCARFTYGGCYGNKNNFEEEQQCLE 423

Qy     155 RC--------FRQQENPPLP 166
           |         |  :   |:|
Db     424 SCRGISKKDVFGLRREIPIP 443


RESULT   7
Q9R097
ID   Q9R097      PRELIMINARY;      PRT;   507 AA.
AC   Q9R097;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 1.
GN   SPINT1 OR HAI1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Itoh H., Kataoka H., Koono H.;
RT   "Mouse hepatocyte growth factor activator inhibitor type 1 (HAI-1).";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF099018; AAF02490.1; -.
DR   HSSP; P05067; 1TAW.
DR   MGD; MGI:1338033; Spint1.
DR   INTERPRO; IPR002172; -.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PFAM; PF00057; ldl_recept_a; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 2.
DR   PROSITE; PS50068; LDLRA_2; 1.
SQ   SEQUENCE   507 AA;  56676 MW;  20CB5DEDCEF46AA7 CRC64;

  Query Match           31.0%;  Score 294;  DB 11;  Length 507;
  Best Local Similarity  33.1%;  Pred. No. 1.2e-23;
  Matches   59;  Conservative   23;  Mismatches   66;  Indels   30;  Gaps    3;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATV---- 64
           |:|| |  |||| | |||:|:  :  |: | :||| || |||| :|||:  |  |
Db     242 DYCLASYKVGRCRGSFPRWYYDPKEQICKSFTFGGCLGNKNNYLREEECMLACKDVQGIS 301

Qy      65 ----------TENATGDLATSRNAAD-----SSVPSAPRRQDSEDHSSDMFNYEE----- 104
                     : :||    ::  : |          |  |   |           ::|
Db     302 PKRHHPVCSGSCHATQFRCSNGCSIDGFLECDDTPDCPDGSDEATCEKYTSGFDELQNIH 361
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Qy     105 ------YCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
                 ||     || |: : ||||::     |  | |||| ||||:: |: |:  |
Db     362 FLSDKGYCAELPDTGFCKENIPRWYYNPFSERCARFTYGGCYGNKNNFEEEQQCLESC 419


RESULT   8
O54819
ID   O54819      PRELIMINARY;      PRT;   306 AA.
AC   O54819;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   TISSUE FACTOR PATHWAY INHIBITOR.
GN   TFPI.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=98152575; PubMed=9493581;
RA   Chang J.-Y., Monroe D.M., Oliver J.A., Liles D.K., Roberts H.R.;
RT   "Cloning, expression, and characterization of mouse tissue factor
RT   pathway inhibitor (TFPI).";
RL   Thromb. Haemost. 79:306-309(1998).
DR   EMBL; AF004833; AAC40035.1; -.
DR   HSSP; P10646; 1TFX.
DR   MGD; MGI:1095418; Tfpi.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 3.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 3.
KW   Serine protease inhibitor.
SQ   SEQUENCE   306 AA;  34987 MW;  D3EA3297E4B6A359 CRC64;


  Query Match             27.4%;  Score 259.5;  DB 11;  Length 306;
  Best Local Similarity   33.3%;  Pred. No. 3.6e-20;
  Matches   55;  Conservative   21;  Mismatches   64;  Indels   25;  Gaps    3;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCAT----- 63
           ||| : :  | ||  | |: ||     |: |||||| || ||: | :|| | |
Db     119 DFCFLEEDPGLCRGYMKRYLYNNQTKQCERFVYGGCLGNRNNFETLDECKKICENPVHSP 178

Qy      64 -----------VTE-NATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAV 111
                      ||: |   | :|  |       |  |||:|        :    :|   |
Db     179 SPVNEVQMSDYVTDGNTVTDRSTVNNIVVPQSPKVPRRRD--------YRGRPWCLQPAD 230

Qy     112 TGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           :| |:||  |:|::     |: | | || || |:: :   |:  |
Db     231 SGLCKASERRFYYNSATGKCHRFNYTGCGGNNNNFTTRRRCLRSC 275


RESULT   9
Q9VAV4
ID   Q9VAV4      PRELIMINARY;      PRT;  2230 AA.
AC   Q9VAV4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   CG18436 PROTEIN.
GN   CG18436.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003765; AAF56794.1; -.
DR   HSSP; P12111; 2KNT.
DR   FLYBASE; FBgn0039586; CG18436.
DR   INTERPRO; IPR000884; -.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 10.
DR   PFAM; PF00090; tsp_1; 5.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 9.
SQ   SEQUENCE   2230 AA;  239721 MW;  F026C96035B4F5BD CRC64;


  Query Match             27.3%;  Score 259;  DB 5;  Length 2230;
  Best Local Similarity   32.9%;  Pred. No. 3.4e-19;
  Matches   52;  Conservative   16;  Mismatches   66;  Indels   24;  Gaps    3;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :   || |   :  |:|:  | :|: | |||| || | : |:| || :|    |
Db    1807 DICEIPAEVGECANYVTSWYYDTQDQACRQFYYGGCGGNENRFPTEESCLARCDRKPEPT 1866

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
           |   ||       | |||             |      | |     :|:|| :
Db    1867 TTTPATR---------PQPSRQD------------VCDEEPAPGECSTWVLKWHFDRKI 1904

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLP 166
           :|  | || | || | : :|  |  ||  |:  || |
Db    1905 GACRQFYYGNCGGNGNRFETENDCQQRCLSQE--PPAP 1940


RESULT  10
O44938
ID   O44938      PRELIMINARY;      PRT;   972 AA.
AC   O44938;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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```
DE   THROMBOSPONDIN-LIKE PROTEIN (FRAGMENT).
GN   THR1.
OS   Haemonchus contortus.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC   Trichostrongyloidae; Haemonchidae; Haemonchinae; Haemonchus.
OX   NCBI_TaxID=6289;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MOREDUN;
RA   Newlands G.F.J., Skuce P.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF043121; AAB99830.1; -.
DR   HSSP; P05067; 1TAW.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 6.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 6.
[redacted]   Serine protease inhibitor.
     NON_TER       1       1
     SEQUENCE   972 AA;  105301 MW;  4465C6BEB8DC19ED CRC64;

  Query Match             27.1%;  Score 256.5;  DB 5;  Length 972;
  Best Local Similarity   30.1%;  Pred. No. 2.6e-19;
  Matches   47;  Conservative   21;  Mismatches   61;  Indels   27;  Gaps    1;

Qy      11 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENATG 70
           | :   ||:|: |   |:| :  |||  | | || ||:| : ::|||   |
Db     794 CHLPLDVGKCQGSFDSWYYEMATGSCVEFKYSGCSGNANRFASREECENTCV-------- 845

Qy      71 DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVERNS 130
                        : || ||    :    |     ||||     :||::    :
Db     846 ------------------RHSEPHSDTTSHGTSVCDEAKETGPCTNFATKWYYNKADGT 886

Qy     131 CNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLP 166
           || | |||| | :| : :|::|   |   |:   ||
Db     887 CNRFHYGGCEGTRNRFDNEQSCKAACANHQDACTLP 922


RESULT  11
Q9U8G8
ID   Q9U8G8      PRELIMINARY;      PRT;  3198 AA.
AC   Q9U8G8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   LACUNIN PRECURSOR.
OS   Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Sphingiodea; Sphingidae; Sphinginae; Manduca.
OX   NCBI_TaxID=7130;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99457716; PubMed=10528409;
RA   Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
RT   "Expression of lacunin, a large multidomain extracellular matrix
RT   protein, accompanies morphogenesis of epithelial monolayers in Manduca
RT   sexta.";
RL   Insect Biochem. Mol. Biol. 29:883-897(1999).
DR   EMBL; AF078161; AAF04457.1; -.
DR   HSSP; P12111; 2KNT.
DR   INTERPRO; IPR000884; -.
DR   INTERPRO; IPR002221; -.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR003006; -.
DR   PFAM; PF00014; Kunitz_BPTI; 10.
DR   PFAM; PF00047; ig; 2.
DR   PFAM; PF00095; wap; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 8.
DR   PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
SQ   SEQUENCE   3198 AA;  349366 MW;  AB4ACD459C0D9134 CRC64;

  Query Match             26.9%;  Score 255;  DB 5;  Length 3198;
  Best Local Similarity   31.7%;  Pred. No. 1.4e-18;
  Matches   51;  Conservative   23;  Mismatches   63;  Indels   24;  Gaps    3;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :   :| |     ||:|:  : ||| | |||| || ||: |: ||  :|
Db    2133 DLCTLPAAIGDCADYRERWYYDTREKSCQRFYYGGCAGNGNNFATQAECEGRC------- 2185

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                   ::: : :  |   :| |        | |       |||  :  || :| :
Db    2186 ----------SEAKITTTVR--PTEAHP-----LTEMCFMEKDPGPCTDTETRWVYDYKL 2228

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGS 169
             |  | |||| ||:|:: :|| |   |   |:   ||: |
Db    2229 GKCVTFEYGGCGGNRNNFPTEEYCQYYCGTAQDICQLPMRS 2269


RESULT  12
O93424
ID   O93424      PRELIMINARY;      PRT;  287 AA.
AC   O93424;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   HYPOTHETICAL 33.1 KDA PROTEIN.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RA   Gracey A.Y.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF008648; AAC19410.1; -.
DR   HSSP; P31713; 1SHP.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 3.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 3.
KW   Hypothetical protein; Serine protease inhibitor.
SQ   SEQUENCE   287 AA;  33093 MW;  DF69B3D76718115E CRC64;

  Query Match             26.6%;  Score 252;  DB 13;  Length 287;
  Best Local Similarity   30.9%;  Pred. No. 2.1e-19;
  Matches   50;  Conservative   19;  Mismatches   53;  Indels   40;  Gaps    3;

Qy       8 HDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTEN 67
           |  | : |  | |:|   |::::   | |: | |||| || ||: | :|| | |
Db      39 HHSCALKKDEGPCKALKDRFYFDTDTGRCESFEYGGCQGNENNFETLQECEKMCLV---- 94

Qy      68 ATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVE 127
                                    || |         |  :   ||||   ||::|| :
Db      95 ----------------------KEDKSP--------CQLDDEPGPCRGLVPRYFFDFK 122

Qy     128 RNSCNNFIYGGCRGNKNSYRSEEACMLRCF----RQQENPPL 165
             |  | |||| || |:::: : |  ||       : | ||
Db     123 SQECKRFFYGGCFGNANNFKTIKECHERCLPALNNMERNAPL 164


RESULT  13
O76840
ID   O76840      PRELIMINARY;      PRT;  2167 AA.
AC   O76840; Q22911;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
```

```
DE   C37C3.6 PROTEIN.
GN   C37C3.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Geisel C., Bradshaw H.;
RT   "The sequence of C. elegans cosmid C37C3.";
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) MAY BE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN IS THAT
CC       OF FORM B.
DR   EMBL; U64857; AAC25868.1; -.
DR   EMBL; U64857; AAC25867.1; -.
DR   HSSP; P00981; 1DTK.
DR   INTERPRO; IPR000884; -.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR003006; -.
DR   PFAM; PF00014; Kunitz_BPTI; 11.
DR   PFAM; PF00047; ig; 1.
DR   PFAM; PF00090; tsp_1; 6.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 10.
KW   Serine protease inhibitor; Hypothetical protein; Alternative splicing.
FT   VARSPLIC    147    155       MISSING (IN ISOFORM A).
FT   VARSPLIC   1556   1558       KDD -> SKF (IN ISOFORM A).
FT   VARSPLIC   1559   2167       MISSING (IN ISOFORM A).
SQ   SEQUENCE   2167 AA;  237599 MW;  96274786D52E3639 CRC64;

  Query Match           26.4%;  Score 250.5;  DB 5;  Length 2167;
  Best Local Similarity 30.1%;  Pred. No. 2.7e-18;
  Matches   49;  Conservative   26;  Mismatches   79;  Indels    9;  Gaps    1;

Qy       5 RSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC--- 61
           :|: | |   :  | |     :|:||     |: | |||| || | : :|:|| ::|
Db    1265 QSMEDICRSRQDAGPCETYSDQWFYNAFSQECETFTYGGCGGNLNRFRSKDECEQRCFFV 1324

Qy      62 ------ATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPC 115
                |   | |      :: |  |:: | |::  |           : |  |   | |
Db    1325 HGAQPSAARQEQAQPAAQPAQPAQPSNIVSPPQQSASPVVVPSNSKQRDACHLNVDQGRC 1384

Qy     116 RASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFR 158
           : :|  ||::|   ||  | | || || | : |:: |   | :
Db    1385 KGAFDSWYYEVATGSCVTFKYTGCGGNANRFASKDQCESLCVK 1427


RESULT  14
P78491
ID   P78491      PRELIMINARY;      PRT;   151 AA.
AC   P78491;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   ALPHA-1-MICROGLOBULIN (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91214554; PubMed=1708673;
RA   Vetr H., Gebhard W.;
RT   "Structure of the human alpha 1-microglobulin-bikunin gene.";
RL   Biol. Chem. Hoppe-Seyler 371:1185-1196(1990).
DR   EMBL; X54818; CAA38587.1; -.
DR   EMBL; X54816; CAA38587.1; JOINED.
DR   HSSP; P02760; 1BIK.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 2.
KW   Serine protease inhibitor.
FT   NON_TER      1      1
SQ   SEQUENCE   151 AA;  16542 MW;  88F400C5ECA19831 CRC64;

  Query Match           25.8%;  Score 244.5;  DB 4;  Length 151;
  Best Local Similarity 32.4%;  Pred. No. 6.9e-19;
  Matches   48;  Conservative   14;  Mismatches   47;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
             | | :    | |     |::|| |  :|: | |||| || ||::|::|||: | ||
Db      28 DSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRTVAA-- 85

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                |    | |||||    | ||  :
Db      86 -----------------------------------CNLPIVRGPCRAFIQLWAFDAVK 108

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     109 GKCVLFPYGGCQGNGNKFYSEKECREYC 136


RESULT  15
O45881
ID   O45881      PRELIMINARY;      PRT;  2225 AA.
AC   O45881;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   W01F3.3 PROTEIN.
GN   W01F3.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cummings P.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94150718; PubMed=7906398;
RA   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA   Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA   Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA   Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA   Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA   Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA   Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA   Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA   Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
DR   EMBL; Z92815; CAB07294.1; -.
DR   HSSP; P31713; 1SHP.
DR   INTERPRO; IPR000716; -.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 10.
DR   PFAM; PF00086; thyroglobulin_1; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 8.
DR   PROSITE; PS00484; THYROGLOBULIN_1; UNKNOWN_1.
KW   Serine protease inhibitor.
SQ   SEQUENCE   2225 AA;  242197 MW;  A5DD8AE9D2A7B02A CRC64;

  Query Match           25.3%;  Score 240;  DB 5;  Length 2225;
  Best Local Similarity 29.3%;  Pred. No. 3.8e-17;
  Matches   46;  Conservative   21;  Mismatches   58;  Indels   32;  Gaps    2;
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Qy      11 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKC--ATVTENA 68
           ||  :  | ||    ||:::    :| :| | || || ||: :||||:  |     | :|
Db     777 CLHPRDSGNCRGQFVRWFFDDEKKNCDVFTYTGCQGNGNNFASKEECMAICHKPEPTPSA 836

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
           | |                              : : |: :   | |   | |: || |
Db     837 TPD-----------------------------FSQVCSNDVDAGECNGVFERFAFDAEA 866

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPL 165
             |  | |||| || |:: : : |  ||    :  |:
Db     867 QDCRAFTYGGCGGNGNNFATMQECRSRCVMAMKKSPV 903
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Search completed: January 31, 2001, 15:04:15
Job time: 91 sec

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Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 197
```

RESULT 2
O00271
ID O00271 PRELIMINARY; PRT; 252 AA.
AC O00271;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE BIKUNIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
[redacted] TISSUE=PLACENTA;
[redacted] MEDLINE=97277372; PubMed=9115294;
RA Marlor C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M.,
RA Tamburini P.P.;
RT "Identification and cloning of human placental bikunin, a novel serine
RT protease inhibitor containing two Kunitz domains.";
RL J. Biol. Chem. 272:12202-12208(1997).
DR EMBL; U78095; AAC02781.1; -.
DR HSSP; P05067; 1TAW.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ; 2.
KW Serine protease inhibitor.
SQ SEQUENCE 252 AA; 28228 MW; A7D3360C0EECAB2B CRC64;

Query Match 100.0%; Score 948; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.7e-94;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 197
```

RESULT 3
O14895
ID O14895 PRELIMINARY; PRT; 252 AA.
AC O14895;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE KUNITZ-TYPE PROTEASE INHIBITOR.
GN KOP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREATIC CANCER;
RA Mueller-Pillasch F., Wallrapp C., Bartels K., Varga G., Friess H.,
RA Buechler M., Adler G., Gress T.M.;
RL Biochim. Biophys. Acta 0:0-0(1997).
DR EMBL; AF027205; AAB84031.1; -.
DR HSSP; P05067; 1TAW.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ; 2.
KW Protease; Serine protease inhibitor.
SQ SEQUENCE 252 AA; 28231 MW; B21593466413841E CRC64;

Query Match 99.7%; Score 945; DB 4; Length 252;
Best Local Similarity 99.4%; Pred. No. 3.5e-94;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db      28 ADRERSIHDFCLVSKVVGRCRASMPKWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 197
```

RESULT 4
Q9WU03
ID Q9WU03 PRELIMINARY; PRT; 252 AA.
AC Q9WU03;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2.
GN HAI2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=99160423; PubMed=10049781;
RA Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
RT "Hepatocyte growth factor activator inhibitor type 2 lacking the first
RT Kunitz-type serine proteinase inhibitor domain is a predominant
RT product in mouse but not in human.";
RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
DR EMBL; AF099016; AAD22172.1; -.
DR HSSP; P05067; 1TAW.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ; 2.
KW Serine protease inhibitor.
SQ SEQUENCE 252 AA; 27914 MW; B2FF4B86924D4F8F CRC64;

Query Match 69.9%; Score 663; DB 11; Length 252;
Best Local Similarity 68.2%; Pred. No. 9e-64;
Matches 116; Conservative 21; Mismatches 33; Indels 0; Gaps 0;

```
Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           | ||  :|: | |||||:||||:||||||:|||||| ||||||:|| ||| :|||||
Db      28 ASRELDVHESCGVSKVVGKCRASIPRWWYNITDGSCQPFVYGGCEGNGNNYQSKEECLDK 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           || |||| | |:| :|| ||||| | ||:| :|| |:::|||||||   ||||||||:||
Db      88 CAGVTENTTDDMARNRNGADSSVLSVPRKQSAEDLSAEIFNYEEYCVPKAVTGPCRAAFP 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           |||:| |:||| :|||||||||||||| |:|||| |  :| :| |  | |
Db     148 RWYYDTEKNSCISFIYGGCRGNKNSYLSQEACMQHCSGKQMHPFLTPGLK 197
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 31, 2001, 15:02:44 ; Search time 23.18 Seconds
(without alignments)
859.592 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 948
Sequence: 1 ADRERSIHDFCLVSKVVGRC.....ACMLRCFRQQENPPLPLGSK 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

[redacted]tal number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	948	100.0	252	4	O43291	O43291 homo sapien
2	948	100.0	252	4	O00271	O00271 homo sapien
3	945	99.7	252	4	O14895	O14895 homo sapien
4	663	69.9	252	11	Q9WU03	Q9wu03 mus musculu
5	381	40.2	195	11	Q9WU04	Q9wu04 mus musculu
6	312	32.9	513	4	O43278	O43278 homo sapien
7	294	31.0	507	11	Q9R097	Q9r097 mus musculu
8	259.5	27.4	306	11	O54819	O54819 mus musculu
9	259	27.3	2230	5	Q9VAV4	Q9vav4 drosophila
10	256.5	27.1	972	5	O44938	O44938 haemonchus
11	255	26.9	3198	5	Q9U8G8	Q9u8g8 manduca sex
12	252	26.6	287	13	O93424	O93424 cyprinus ca
13	250.5	26.4	2167	5	O76840	O76840 caenorhabdi
14	244.5	25.8	151	4	P78491	P78491 homo sapien
15	240	25.3	2225	5	O45881	O45881 caenorhabdi
16	239.5	25.3	396	6	Q28874	Q28874 canis famil
17	235.5	24.8	144	11	Q9QW87	Q9qw87 mesocricetu
18	233.5	24.6	352	11	O70160	O70160 cavia porce
19	228	24.1	251	4	O95103	O95103 homo sapien
20	227.5	24.0	246	11	Q9Z2U8	Q9z2u8 mus musculu
21	222	23.4	1043	5	O17644	O17644 caenorhabdi
22	219.5	23.2	342	13	P70004	P70004 xenopus lae
23	219	23.1	922	5	Q21418	Q21418 caenorhabdi
24	209	22.0	1743	5	Q9XWX5	Q9xwx5 caenorhabdi
25	208	21.9	751	11	Q60709	Q60709 mus musculu
26	208	21.9	763	11	Q61482	Q61482 mus musculu
27	204.5	21.6	230	11	O35536	O35536 mus musculu
28	200	21.1	523	4	Q14594	Q14594 homo sapien
29	200	21.1	1599	5	Q09983	Q09983 caenorhabdi
30	199	21.0	1522	5	Q22685	Q22685 caenorhabdi
31	198	20.9	1195	5	Q9N343	Q9n343 caenorhabdi
32	195	20.6	1391	5	Q19021	Q19021 caenorhabdi
33	194	20.5	1297	5	Q9U350	Q9u350 caenorhabdi
34	193	20.4	1474	5	O62504	O62504 caenorhabdi
35	186.5	19.7	747	13	Q91963	Q91963 xenopus lae
36	186	19.6	484	4	Q13793	Q13793 homo sapien
37	186	19.6	547	4	Q13764	Q13764 homo sapien
38	186	19.6	770	6	Q9TUI0	Q9tui0 sus scrofa
39	185.5	19.6	1203	5	O45916	O45916 caenorhabdi
40	183	19.3	160	11	Q9QZ78	Q9qz78 cavia sp.
41	178	18.8	1965	5	O61893	O61893 caenorhabdi
42	177	18.7	59	5	Q9TWF8	Q9twf8 anemonia s
43	174.5	18.4	692	5	O45101	O45101 caenorhabdi
44	174.5	18.4	780	13	O73683	O73683 tetraodon
45	173	18.2	58	5	Q9TWF9	Q9twf9 anemonia su

ALIGNMENTS

RESULT 1
O43291
ID O43291 PRELIMINARY; PRT; 252 AA.
AC O43291;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98010584; PubMed=9346890;
RA Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K.,
RA Kitamura N.;
RT "Purification and cloning of hepatocyte growth factor activator
RT inhibitor type 2, a Kunitz-type serine protease inhibitor.";
RL J. Biol. Chem. 272:27558-27564(1997).
DR EMBL; AB006534; BAA25024.1; -.
DR HSSP; P05067; 1TAW.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ; 2.
KW Serine protease inhibitor.
SQ SEQUENCE 252 AA; 28169 MW; F7D3D834ED631DF0 CRC64;

Query Match 100.0%; Score 948; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.7e-94;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
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Db      28 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 147
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 31, 2001, 15:02:39 ; Search time 16.59 Seconds
(without alignments)
350.388 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 948
Sequence: 1 ADRERSIHDFCLVSKVVGRC.....ACMLRCFRQQENPPLPLGSK 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*
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2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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4: /SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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11: /SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:*
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18: /SIDS1/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	948	100.0	170	18	W30041	Human placental bi
2	948	100.0	179	18	W30053	Human placental bi
3	948	100.0	197	18	W30043	Human placental bi
4	948	100.0	213	18	W30042	Human placental bi
5	948	100.0	225	18	W30046	Human placental bi
6	948	100.0	235	18	W30060	Human consensus bi
7	948	100.0	240	18	W30045	Human placental bi
8	948	100.0	248	18	W30044	Human consensus bi
9	948	100.0	252	18	W30040	Human placental bi
10	948	100.0	252	18	W13665	Hepatocyte growth
11	948	100.0	252	19	W70286	Human tissue facto
12	859	90.6	153	18	W30051	Human placental bi
13	819	86.4	146	18	W30052	Human placental bi
14	750	79.1	170	18	W30061	Human consensus bi
15	501	52.8	92	18	W30054	Human placental bi
16	488	51.5	130	18	W30062	EST R35464 protein
17	487	51.4	169	18	W30063	EST R74593 protein
18	337	35.5	58	18	W30049	Human placental bi
19	334	35.2	58	18	W30047	Human placental bi
20	312	32.9	513	18	W27368	Hepatocyte growth
21	312	32.9	513	20	W92653	Human HAI-1 protei
22	297	31.3	51	18	W30048	Human placental b
23	297	31.3	51	18	W30050	Human placental bi
24	281	29.6	128	20	W82768	Bovine bikunin pep
25	277	29.2	128	20	W82764	Bovine bikunin pe
26	276	29.1	129	20	W82765	Bovine bikunin pep
27	274	28.9	128	20	W82766	Bovine bikunin pep
28	273	28.8	128	20	W82769	Bovine bikunin pep
29	272.5	28.7	124	18	W25933	New protease inhib
30	272.5	28.7	144	18	W25938	SUC2-Ep7-d21-RPDF
31	272	28.7	128	20	W82787	Bovine bikunin pep
32	272	28.7	128	20	W82767	Bovine bikunin pep
33	272	28.7	128	20	W82771	Bovine bikunin pep
34	271.5	28.6	124	18	W25932	New protease inhib
35	271.5	28.6	144	18	W25936	SUC2-Ep1-d21-RPDF-
36	271.5	28.6	145	18	W25935	Novel protease inh
37	271.5	28.6	165	18	W25937	Elastase inhibitor
38	267	28.2	128	20	W82788	Bovine bikunin pe
39	267	28.2	128	20	W82770	Bovine bikunin pe
40	266.5	28.1	560	15	R62523	Hookworm anticoa
41	265	28.0	128	20	W82772	Bovine bikunin pe
42	261	27.5	128	20	W82784	Bovine bikunin pe
43	259	27.3	128	20	W82783	Bovine bikunin pep
44	255	26.9	128	20	W82785	Bovine bikunin pe
45	254.5	26.8	124	17	R92233	Human mature alph

ALIGNMENTS

RESULT 1
W30041
ID W30041 standard; Protein; 170 AA.
XX
AC W30041;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470875/43.
XX

PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 65; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 170 AA;

Query Match 100.0%; Score 948; DB 18; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 60

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 120

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 170
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RESULT 2
W30053
ID W30053 standard; Protein; 179 AA.
XX
AC W30053;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 67; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 179 AA;

Query Match 100.0%; Score 948; DB 18; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.3e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 60

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 120

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 170
```

RESULT 3
W30043
ID W30043 standard; Protein; 197 AA.
XX
AC W30043;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX

PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 65; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 948; DB 18; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.4e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
Db 19 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 78

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
Db 79 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 138

Qy 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
Db 139 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 188

RESULT 4
W30042
ID W30042 standard; Protein; 213 AA.
XX
AC W30042;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 65; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cor[redacted]
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 213 AA;

Query Match 100.0%; Score 948; DB 18; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.6e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK
Db 1 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
Db 61 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp

Qy 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
Db 121 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 170

RESULT 5
W30046
ID W30046 standard; Protein; 225 AA.

```
XX
AC   W30046;
XX
DT   20-APR-1998  (first entry)
XX
DE   Human placental bikunin.
XX
KW   Human; placental bikunin; inhibition; trypsin; kallikrein;
KW   plasmin; factor XIIa; treatment; prevention; oedema;
KW   inflammation; infection; granulomatosis; multiple sclerosis;
KW   ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW   blood coagulation disease; polytrauma; stroke; haemorrhage;
KW   gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS   Homo sapiens.
XX
PN   WO9733996-A2.
XX
PD   18-SEP-1997.
XX
PF   10-MAR-1997;   97WO-US03894.
XX
PR   04-OCT-1996;   96US-0725251.
PR   11-MAR-1996;   96US-0013106.
PR   14-JUN-1996;   96US-0019793.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Davis G,  Delaria KA,  Marlor CW,  Muller DK,  Tamburini PP;
XX
DR   WPI; 1997-470876/43.
XX
PT   New human placental bikunin - used to inhibit kallikrein, trypsin
PT   etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT   perioperative blood loss
XX
PS   Claim 1; Page 66; 110pp; English.
XX
CC   The present sequence is a human placental bikunin, which
CC   inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC   Bikunin can be used to treat or prevent brain and spinal cord
CC   oedema, inflammation, infection or granulomatosis, multiple
CC   sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC   fibrosis, blood coagulation diseases, polytrauma, stroke,
CC   cerebral or subarachnoid haemorrhage and gastric or cervical
CC   cancer and prevent metastasis. It is particularly useful for
CC   reducing blood loss during surgery, and can also be used to treat
CC   other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC   influenza and similar viral infections, acute pancreatitis and
CC   gout, and prevent pre-term labour. It has similar properties to
CC   aprotinin, but is less highly charged so should be less
CC   immunogenic and less likely to damage the kidneys. Manipulation
CC   of the bikunin sequence may allow the inhibitory profile to be
CC   altered. It also reduces or eliminates the need for whole donor
CC   blood or blood products during surgery, thereby reducing the risk
CC   of infection and other adverse side effects, as well as reducing
CC   the cost of surgery.
XX
SQ   Sequence   225 AA;

  Query Match             100.0%;  Score 948;  DB 18;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-89;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 60

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 120

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 170

RESULT   6
W30060
ID   W30060 standard; Protein; 235 AA.
XX
AC   W30060;
XX
DT   20-APR-1998  (first entry)
XX
DE   Human consensus bikunin.
XX
KW   Human; consensus bikunin; inhibition; trypsin; kallikrein;
KW   plasmin; factor XIIa; treatment; prevention; oedema;
KW   inflammation; infection; granulomatosis; multiple sclerosis;
KW   ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW   blood coagulation disease; polytrauma; stroke; haemorrhage;
KW   gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 198
FT                   /note= "encoded by TGA"
FT   Misc-difference 201
FT                   /note= "encoded by TGA"
FT   Misc-difference 226
FT                   /note= "encoded by GAN"
FT   Misc-difference 233
FT                   /note= "encoded by TGA"
XX
PN   WO9733996-A2.
XX
PD   18-SEP-1997.
XX
PF   10-MAR-1997;   97WO-US03894.
XX
PR   04-OCT-1996;   96US-0725251.
PR   11-MAR-1996;   96US-0013106.
PR   14-JUN-1996;   96US-0019793.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Davis G,  Delaria KA,  Marlor CW,  Muller DK,  Tamburini PP;
XX
DR   WPI; 1997-470876/43.
DR   N-PSDB; T90732.
XX
PT   New human placental bikunin - used to inhibit kallikrein, trypsin
PT   etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT   perioperative blood loss
XX
PS   Disclosure; Fig 3; 110pp; English.
XX
CC   The present sequence is a consensus human bikunin, which
CC   inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC   Bikunin can be used to treat or prevent brain and spinal cord
CC   oedema, inflammation, infection or granulomatosis, multiple
CC   sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC   fibrosis, blood coagulation diseases, polytrauma, stroke,
CC   cerebral or subarachnoid haemorrhage and gastric or cervical
CC   cancer and prevent metastasis. It is particularly useful for
CC   reducing blood loss during surgery, and can also be used to treat
CC   other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC   influenza and similar viral infections, acute pancreatitis and
CC   gout, and prevent pre-term labour. It has similar properties to
CC   aprotinin, but is less highly charged so should be less
CC   immunogenic and less likely to damage the kidneys. Manipulation
CC   of the bikunin sequence may allow the inhibitory profile to be
CC   altered. It also reduces or eliminates the need for whole donor
```

CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 235 AA;

Query Match 100.0%; Score 948; DB 18; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.8e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
Db 19 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 78

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
Db 79 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 138

Qy 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
Db 139 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 188

RESULT 7
W30045
ID W30045 standard; Protein; 240 AA.
XX
AC W30045;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
DR N-PSDB; T90734.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 66; 110pp; English.
XX
CC The present sequence is human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 240 AA;

Query Match 100.0%; Score 948; DB 18; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.8e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
Db 28 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 87

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
Db 88 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 147

Qy 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
Db 148 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 197

RESULT 8
W30044
ID W30044 standard; Protein; 248 AA.
XX
AC W30044;
XX
DT 20-APR-1998 (first entry)
XX
DE Human consensus bikunin.
XX
KW Human; consensus bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470875/43.
DR N-PSDB; T90733.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX

PS Claim 1; Page 66; 110pp; English.
XX
CC The present sequence is a consensus human bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 948; DB 18; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
Db 24 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 83

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
Db 84 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 143

Qy 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
Db 144 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 193

RESULT 9
W30040
ID W30040 standard; Protein; 252 AA.
XX
AC W30040;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
DR N-PSDB; T90731.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 65; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 252 AA;

Query Match 100.0%; Score 948; DB 18; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.9e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
Db 28 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 87

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
Db 88 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 147

Qy 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
Db 148 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 197

RESULT 10
W13665
ID W13665 standard; Protein; 252 AA.
XX
AC W13665;
XX
DT 11-NOV-1997 (first entry)
XX
DE Hepatocyte growth factor activator inhibitor HAI-II.
XX
KW Hepatocyte growth factor activator inhibitor; HAI-II; HGF; human;
KW protease inhibitor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= Sig_peptide
FT Protein 28..252
FT /label= Mat_protein
XX
PN EP758682-A2.

XX
PD 19-FEB-1997.
XX
PF 23-JUL-1996; 96EP-0111861.
XX
PR 24-JUL-1995; 95JP-0187134.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
PI Kawaguchi T, Kitamura N, Shimomura T;
XX
DR WPI; 1997-134770/13.
DR N-PSDB; T61439.
XX
PT Novel protein HAI-II - inhibits protease activity of hepatocyte
PT growth factor activator
XX
PS Claim 4; Page 18-19; 24pp; English.
XX
CC This sequence comprises a novel protein, designated HAI-II,
CC that inhibits the protease activity of hepatocyte growth factor
CC (HGF) activator. The sequence was deduced from a cDNA clone
CC (T61439) obtained from cancer cell line MKN45. Also claimed
CC are isolated peptides (W13662-64) of HAI-II, the DNA encoding
CC HAI-II, a vector carrying this DNA, and a host cell, pref. an
CC animal cell, transformed with the vector. HAI-II can be used for
CC regulating HGF activator activity (and thus HGF activity) in vitro
CC and in vivo. It may also be used for investigating the function of
CC HAI-II in vivo and the effect of HAI-II in hepatic disorders.
XX
SQ Sequence 252 AA;

Query Match 100.0%; Score 948; DB 18; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.9e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 197
```

RESULT 11
W70286
ID W70286 standard; Protein; 252 AA.
XX
AC W70286;
XX
DT 06-NOV-1998 (first entry)
XX
DE Human tissue factor pathway inhibitor-3 (TFPI-3).
XX
KW Human tissue factor pathway inhibitor-3; TFPI-3; blood clot; sepsis;
KW fibrin clot; coronary occlusion; acute myocardial infarction;
KW prophylaxis; peripheral arterial embolism; inflammatory disease;
KW transplant rejection; anticoagulant; blood transfusion;
KW extracorporeal circulation; dialysis; haemophili; kunitz type domain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT /note= "Signal peptide"
FT Protein 28..252
FT /note= "TFPI-3"

XX
PN WO9833920-A2.
XX
PD 06-AUG-1998.
XX
PF 27-JAN-1998; 98WO-US01468.
XX
PR 31-JAN-1997; 97US-0036703.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Gentz RL, Hsu T, Ni J, Rosen CA;
XX
DR WPI; 1998-437473/37.
DR N-PSDB; V33063.
XX
PT Isolated tissue factor pathway inhibitor-3 - used to develop
PT products for treating, e.g. pulmonary embolism, thrombosis, sepsis,
PT inflammatory disease, transplant rejection or haemophilia
XX
PS Disclosure; Fig 1A-1B; 57pp; English.
XX
CC The present sequence represents a human tissue factor pathway
CC inhibitor-3 (TFPI-3) which contains two kunitz type domains. The
CC invention also provides the TFPI-3 cDNA and screening methods for
CC identifying agonists and antagonists of TFPI-3. As TFPI-3 inhibits
CC protease activity, it is claimed to be useful for, e.g. inhibiting
CC intravascular clotting and preventing the formation of fibrin clots
CC both in vitro and in vivo, for treating coronary occlusion with acute
CC myocardial infarction and in the prophylaxis and treatment of
CC peripheral arterial embolism, for the treatment of sepsis, inflammatory
CC diseases and transplant rejection. TFPI-3 is also claimed to be useful
CC as an anticoagulant in blood transfusions, extracorporeal circulation,
CC and dialysis procedures and in blood samples for laboratory purposes.
CC The TFPI-3 antagonists are claimed to be useful for promoting
CC coagulation, e.g. in the treatment of haemophilia.
XX
SQ Sequence 252 AA;

Query Match 100.0%; Score 948; DB 19; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.9e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 197
```

RESULT 12
W30051
ID W30051 standard; Protein; 153 AA.
XX
AC W30051;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.

XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 67; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 153 AA;

Query Match 90.6%; Score 859; DB 18; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.3e-80;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       7 IHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTE 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkkcatvte 60

Qy      67 NATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDV 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 natgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfprwyfdv 120

Qy     127 ERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQ 159
          |||||||||||||||||||||||||||||||
Db     121 ernscnnfiyggcrgnknsyrseeacmlrcfrq 153
```

RESULT 13
W30052
ID W30052 standard; Protein; 146 AA.
XX
AC W30052;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 67; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 146 AA;

Query Match 86.4%; Score 819; DB 18; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.6e-76;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      11 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENATG 70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 clvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkkcatvtenatg 60

Qy      71 DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVERNS 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 dlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfprwyfdverns 120

Qy     131 CNNFIYGGCRGNKNSYRSEEACMLRC 156
           |||||||||||||||||||||||||
Db     121 cnnfiyggcrgnknsyrseeacmlrc 146
```

```
RESULT  14
W30061
ID   W30061 standard; Protein; 170 AA.
XX
AC   W30061;
XX
DT   20-APR-1998  (first entry)
XX
DE   Human consensus bikunin.
XX
KW   Human; consensus bikunin; inhibition; trypsin; kallikrein;
KW   plasmin; factor XIIa; treatment; prevention; oedema;
KW   inflammation; infection; granulomatosis; multiple sclerosis;
KW   ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW   blood coagulation disease; polytrauma; stroke; haemorrhage;
KW   gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1..170
FT                   /note= "Xaa = any amino acid, except Cys,
FT                          provided that at least one is different
FT                          from the corresponding native amino acid"
XX
PN   WO9733996-A2.
XX
PD   18-SEP-1997.
XX
PF   10-MAR-1997;   97WO-US03894.
XX
PR   04-OCT-1996;   96US-0725251.
PR   11-MAR-1996;   96US-0013106.
PR   14-JUN-1996;   96US-0019793.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Davis G,  Delaria KA,  Marlor CW,  Muller DK,  Tamburini PP;
XX
DR   WPI; 1997-470876/43.
XX
PT   New human placental bikunin - used to inhibit kallikrein, trypsin
PT   etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT   perioperative blood loss
XX
PS   Disclosure; Page 10; 110pp; English.
XX
CC   The present sequence is a consensus human bikunin, which
CC   inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC   Bikunin can be used to treat or prevent brain and spinal cord
CC   oedema, inflammation, infection or granulomatosis, multiple
CC   sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC   fibrosis, blood coagulation diseases, polytrauma, stroke,
CC   cerebral or subarachnoid haemorrhage and gastric or cervical
CC   cancer and prevent metastasis. It is particularly useful for
CC   reducing blood loss during surgery, and can also be used to treat
CC   other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC   influenza and similar viral infections, acute pancreatitis and
CC   gout, and prevent pre-term labour. It has similar properties to
CC   aprotinin, but is less highly charged so should be less
CC   immunogenic and less likely to damage the kidneys. Manipulation
CC   of the bikunin sequence may allow the inhibitory profile to be
CC   altered. It also reduces or eliminates the need for whole donor
CC   blood or blood products during surgery, thereby reducing the risk
CC   of infection and other adverse side effects, as well as reducing
CC   the cost of surgery.
XX
SQ   Sequence   170 AA;

Query Match             79.1%;  Score 750;  DB 18;  Length 170;
Best Local Similarity   81.2%;  Pred. No. 2.2e-69;
Matches  138;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||| |||||||| | |      |||||||||||| | ||   |||| ||||||||
Db       1 adrersixdfclvskvxgxcxxxxxxwwynvtdgscqlfxyxgcxxxsnnyxtkeeclkk 60

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||| ||||||||||||||||||||||||||||||||||||||| |||||||| | |
Db      61 catxtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyxeyctanavxgxcxxxxx 120

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           |||||||||||| | ||   |||| |||||||||| ||||||||||
Db     121 xwyfdvernscnnfxyxgcxxxknsyxseeacmlrcfrxqenpplplgsk 170


RESULT  15
W30054
ID   W30054 standard; Protein; 92 AA.
XX
AC   W30054;
XX
DT   20-APR-1998  (first entry)
XX
DE   Human placental bikunin.
XX
KW   Human; placental bikunin; inhibition; trypsin; kallikrein;
KW   plasmin; factor XIIa; treatment; prevention; oedema;
KW   inflammation; infection; granulomatosis; multiple sclerosis;
KW   ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW   blood coagulation disease; polytrauma; stroke; haemorrhage;
KW   gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS   Homo sapiens.
XX
PN   WO9733996-A2.
XX
PD   18-SEP-1997.
XX
PF   10-MAR-1997;   97WO-US03894.
XX
PR   04-OCT-1996;   96US-0725251.
PR   11-MAR-1996;   96US-0013106.
PR   14-JUN-1996;   96US-0019793.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Davis G,  Delaria KA,  Marlor CW,  Muller DK,  Tamburini PP;
XX
DR   WPI; 1997-470876/43.
XX
PT   New human placental bikunin - used to inhibit kallikrein, trypsin
PT   etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT   perioperative blood loss
XX
PS   Claim 1; Page 67; 110pp; English.
XX
CC   The present sequence is a human placental bikunin, which
CC   inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC   Bikunin can be used to treat or prevent brain and spinal cord
CC   oedema, inflammation, infection or granulomatosis, multiple
CC   sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC   fibrosis, blood coagulation diseases, polytrauma, stroke,
CC   cerebral or subarachnoid haemorrhage and gastric or cervical
CC   cancer and prevent metastasis. It is particularly useful for
CC   reducing blood loss during surgery, and can also be used to treat
CC   other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC   influenza and similar viral infections, acute pancreatitis and
CC   gout, and prevent pre-term labour. It has similar properties to
CC   aprotinin, but is less highly charged so should be less
CC   immunogenic and less likely to damage the kidneys. Manipulation
CC   of the bikunin sequence may allow the inhibitory profile to be
CC   altered. It also reduces or eliminates the need for whole donor
CC   blood or blood products during surgery, thereby reducing the risk
CC   of infection and other adverse side effects, as well as reducing
```

CC the cost of surgery.
XX
SQ Sequence 92 AA;

Query Match 52.8%; Score 501; DB 18; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 60

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
           |||||||||||||||||||||||||||||||
Db      61 catvtenatgdlatsrnaadssvpsaprrqds 92
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Search completed: January 31, 2001, 15:03:02
Job time: 23 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 31, 2001, 15:03:28 ; Search time 12.37 Seconds
(without alignments)
246.782 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 948
Sequence: 1 ADRERSIHDFCLVSKVVGRC.....ACMLRCFRQQENPPLPLGSK 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	948	100.0	252	1	US-08-685-660A-7	Sequence 7, Appli
2	948	100.0	252	2	US-08-974-196-7	Sequence 7, Appli
3	247.5	26.1	122	2	US-08-422-333-12	Sequence 12, Appl
4	247.5	26.1	122	5	5187153-20	Patent No. 5187153
5	247.5	26.1	122	5	5220013-23	Patent No. 5220013
6	244.5	25.8	143	2	US-08-422-333-10	Sequence 10, Appl
7	244.5	25.8	143	5	5223482-20	Patent No. 5223482
8	244.5	25.8	144	5	5187153-18	Patent No. 5187153
9	244.5	25.8	147	1	US-08-358-160-72	Sequence 72, Appl
10	243.5	25.7	127	5	5466783-24	Patent No. 5466783
11	241.5	25.5	123	5	5466783-21	Patent No. 5466783
12	233.5	24.6	122	5	5223482-22	Patent No. 5223482
13	233.5	24.6	276	1	US-07-828-920A-1	Sequence 1, Appli
14	233.5	24.6	276	1	US-08-437-841-9	Sequence 9, Appli
15	233.5	24.6	276	1	US-08-286-521-9	Sequence 9, Appli
16	233.5	24.6	276	1	US-08-436-175-9	Sequence 9, Appli
17	233.5	24.6	276	2	US-08-796-850-1	Sequence 1, Appli
18	233.5	24.6	276	3	US-08-854-764-3	Sequence 3, Appli
19	233.5	24.6	276	4	PCT-US95-09377-3	Sequence 3, Appli
20	233.5	24.6	276	4	PCT-US95-09464-9	Sequence 9, Appli
21	233.5	24.6	277	1	US-07-844-297-1	Sequence 1, Appli
22	233.5	24.6	304	1	US-08-026-145-2	Sequence 2, Appli
23	233.5	24.6	304	1	US-08-446-646-9	Sequence 9, Appli
24	233.5	24.6	304	1	US-08-676-125A-18	Sequence 18, Appl
25	233.5	24.6	304	2	US-09-136-012A-18	Sequence 18, Appl
26	233.5	24.6	304	3	US-08-676-124-1	Sequence 1, Appli
27	233.5	24.6	304	3	US-08-208-264A-25	Sequence 25, Appl
28	233.5	24.6	304	3	US-09-414-878-1	Sequence 1, Appli
29	233.5	24.6	304	3	US-09-240-136-1	Sequence 1, Appli
30	233.5	24.6	304	5	5466783-2	Patent No. 5466783
31	233.5	24.6	352	3	US-08-854-764-2	Sequence 2, Appli
32	233.5	24.6	352	4	PCT-US95-09377-2	Sequence 2, Appli
33	232.5	24.5	123	5	5466783-22	Patent No. 5466783
34	232	24.5	161	1	US-08-437-841-19	Sequence 19, Appl
35	232	24.5	161	1	US-08-286-521-19	Sequence 19, Appl
36	232	24.5	161	1	US-08-436-175-19	Sequence 19, Appl
37	232	24.5	161	4	PCT-US95-09464-19	Sequence 19, Appl
38	230	24.3	122	5	5466783-23	Patent No. 5466783
39	228	24.1	183	1	US-07-828-920A-5	Sequence 5, Appl
40	226	23.8	189	1	US-07-828-920A-7	Sequence 7, Appl
41	219	23.1	213	5	5466783-25	Patent No. 5466783
42	214.5	22.6	213	2	US-08-796-850-2	Sequence 2, Appl
43	214.5	22.6	235	1	US-08-147-710-2	Sequence 2, Appl
44	214.5	22.6	235	1	US-08-458-090-2	Sequence 2, Appli
45	214.5	22.6	235	2	US-08-457-887-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-08-685-660A-7
; Sequence 7, Application US/08685660A
; Patent No. 5731412
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMOMURA, Takeshi
;    APPLICANT:  KAWAGUCHI, Toshiya
;    APPLICANT:  KITAMURA, Naomi
;    TITLE OF INVENTION:  NOVEL PROTEIN, DNA CODING FOR SAME
;    TITLE OF INVENTION:  AND METHOD OF PRODUCING THE PROTEIN
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/685,660A
;      FILING DATE:  24-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JPA Hei 7-187134
;      FILING DATE:  24-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  Q-42295
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-685-660A-7

  Query Match           100.0%;  Score 948;  DB 1;  Length 252;
  Best Local Similarity  100.0%;  Pred. No. 3e-92;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      28 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 197


RESULT   2
US-08-974-196-7
; Sequence 7, Application US/08974196
; Patent No. 5854396
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMOMURA, Takeshi
;    APPLICANT:  KAWAGUCHI, Toshiya
;    APPLICANT:  KITAMURA, Naomi
     TITLE OF INVENTION:  NOVEL PROTEIN, DNA CODING FOR SAME
     TITLE OF INVENTION:  AND METHOD OF PRODUCING THE PROTEIN
     NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,196
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/685,660
;      FILING DATE:  24-JUL-1996
;      APPLICATION NUMBER:  JPA Hei 7-187134
;      FILING DATE:  24-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  Q-42295
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
   INFORMATION FOR SEQ ID NO:  7:
     SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-974-196-7


  Query Match           100.0%;  Score 948;  DB 2;  Length 252;
  Best Local Similarity  100.0%;  Pred. No. 3e-92;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 197


RESULT   3
US-08-422-333-12
; Sequence 12, Application US/08422333
; Patent No. 5912410
;  GENERAL INFORMATION:
;    APPLICANT:  CORDELL, Barbara L.
;    TITLE OF INVENTION:  TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
;    TITLE OF INVENTION:  THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scios, Inc.
;      STREET:  2450 Bayshore Parkway
;      CITY:  Mountain View
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94043
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/422,333
;      FILING DATE:  13-APR-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shearer, Peter R.
;      REGISTRATION NUMBER:  28,117
;      REFERENCE/DOCKET NUMBER:  21900-28048.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 966-1550
;      TELEFAX:  (415) 968-2438
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  122 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-422-333-12


  Query Match           26.1%;  Score 247.5;  DB 2;  Length 122;
  Best Local Similarity  32.4%;  Pred. No. 6e-19;
  Matches   48;  Conservative   16;  Mismatches   45;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :   | |     |::|| |  :|: |:|||| || ||:|:::|||: | ||
Db       3 DSCQLDYSQGPCLGLFKRYFYNGTSMACETFLYGGCMGNLNNFLSQKECLQTCRTV---- 58

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          | |    | |||||    | ||  :
Db      59 ---------------------------------EACNLPIVQGPCRAFIQLWAFDAVK 83

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : |:: |   |
Db      84 GKCVRFSYGGCKGNGNKFYSQKECKEYC 111


RESULT   4
5187153-20
;Patent No. 5187153
;    APPLICANT: CORDELL, BARBARA;SCHILLING, JAMES W.;KATUNUMA, NOBUHIKO
;    TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
;AMYLOID POLYPEPTIDE DERIVATIVES
;    NUMBER OF SEQUENCES: 33
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/502,273
;      FILING DATE: 29-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 361,912
;      FILING DATE: 06-JUN-1989
```

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;      APPLICATION NUMBER: 359,911
;      FILING DATE: 12-MAY-1989
;      APPLICATION NUMBER: 87,002
;      FILING DATE: 18-AUG-1987
;      APPLICATION NUMBER: 8,810
;      FILING DATE: 30-JAN-1987
;      APPLICATION NUMBER: 948,376
;      FILING DATE: 31-DEC-1986
;      APPLICATION NUMBER: 932,193
;      FILING DATE: 17-NOV-1986
;SEQ ID NO:20:
;      LENGTH: 122
5187153-20


  Query Match             26.1%;  Score 247.5;  DB 5;  Length 122;
  Best Local Similarity   32.4%;  Pred. No. 6e-19;
  Matches   48;  Conservative   16;  Mismatches   45;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |     |::|| |  :|: |:|||| || ||:|:::|||: | ||
Db       3 DSCQLDYSQGPCLGLFKRYFYNGTSMACETFLYGGCMGNLNNFLSQKECLQTCRTV---- 58

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          | |    | |||||    | ||  :
Db      59 ----------------------------------EACNLPIVQGPCRAFIQLWAFDAVK 83

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : |:: |   |
Db      84 GKCVRFSYGGCKGNGNKFYSQKECKEYC 111


RESULT   5
5220013-23
;Patent No. 5220013
;     APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
;     TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
;OF ALZHEIMER'S DISEASE
;     NUMBER OF SEQUENCES: 30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/444,118
;       FILING DATE: 30-NOV-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 87,002
;       FILING DATE: 18-AUG-1987
;       APPLICATION NUMBER: 8,810
;       FILING DATE: 30-JAN-1987
        APPLICATION NUMBER: 948,376
        FILING DATE: 31-DEC-1986
        APPLICATION NUMBER: 932,193
;       FILING DATE: 17-NOV-1986
;SEQ ID NO:23:
;       LENGTH: 122
5220013-23


  Query Match             26.1%;  Score 247.5;  DB 5;  Length 122;
  Best Local Similarity   32.4%;  Pred. No. 6e-19;
  Matches   48;  Conservative   16;  Mismatches   45;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |     |::|| |  :|: |:|||| || ||:|:::|||: | ||
Db       3 DSCQLDYSQGPCLGLFKRYFYNGTSMACETFLYGGCMGNLNNFLSQKECLQTCRTV---- 58

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          | |    | |||||    | ||  :
Db      59 ----------------------------------EACNLPIVQGPCRAFIQLWAFDAVK 83

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : |:: |   |
Db      84 GKCVRFSYGGCKGNGNKFYSQKECKEYC 111


RESULT   6
US-08-422-333-10
; Sequence 10, Application US/08422333
; Patent No. 5912410
;  GENERAL INFORMATION:
;    APPLICANT:  CORDELL, Barbara L.
;    TITLE OF INVENTION:  TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
;    TITLE OF INVENTION:  THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scios, Inc.
;      STREET:  2450 Bayshore Parkway
;      CITY:  Mountain View
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94043
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/422,333
;      FILING DATE:  13-APR-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shearer, Peter R.
;      REGISTRATION NUMBER:  28,117
;      REFERENCE/DOCKET NUMBER:  21900-28048.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 966-1550
;      TELEFAX:  (415) 968-2438
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  143 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-422-333-10


  Query Match             25.8%;  Score 244.5;  DB 2;  Length 143;
  Best Local Similarity   31.8%;  Pred. No. 1.5e-18;
  Matches   47;  Conservative   15;  Mismatches   47;  Indels   39;  Gaps

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |     |::|| |  :|: | |||| || ||::|:::|||: | ||
Db      24 DSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRTVAA-- 81

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          |    : |||||    | ||  :
Db      82 ----------------------------------CNLPVIRGPCRAFIQLWAFDAVK 105

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     105 GKCVLFPYGGCQGNGNKFYSEKECREYC 132


RESULT   7
5223482-20
;Patent No. 5223482
;     APPLICANT: SCHILLING, JAMES W.;PONTE, PHYLLIS A.;CORDELL,
;BARBARA
;     TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
;INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
;     NUMBER OF SEQUENCES: 34
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/361,912
;       FILING DATE: 06-JUN-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 359,911
;       FILING DATE: 12-MAY-1989
;       APPLICATION NUMBER: 87,002
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;       FILING DATE: 18-AUG-1987
;       APPLICATION NUMBER: 8,810
;       FILING DATE: 30-JAN-1987
;       APPLICATION NUMBER: 948,376
;       FILING DATE: 31-DEC-1986
;       APPLICATION NUMBER: 932,193
;       FILING DATE: 17-NOV-1986
;SEQ ID NO:20:
;       LENGTH: 143
5223482-20


  Query Match             25.8%;  Score 244.5;  DB 5;  Length 143;
  Best Local Similarity   31.8%;  Pred. No. 1.5e-18;
  Matches   47;  Conservative   15;  Mismatches   47;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |      |::|| |  :|: | |||| || ||::|::|||: | ||
Db      24 DSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRTVAA-- 81

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          |    : |||||    | ||  :
Db      82 -----------------------------------CNLPVIRGPCRAFIQLWAFDAVK 104

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     105 GKCVLFPYGGCQGNGNKFYSEKECREYC 132


RESULT   8
5187153-18
;Patent No. 5187153
;     APPLICANT: CORDELL, BARBARA;SCHILLING, JAMES W.;KATUNUMA, NOBUHIKO
;     TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
;AMYLOID POLYPEPTIDE DERIVATIVES
;     NUMBER OF SEQUENCES: 33
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/502,273
;       FILING DATE: 29-MAR-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 361,912
;       FILING DATE: 06-JUN-1989
;       APPLICATION NUMBER: 359,911
;       FILING DATE: 12-MAY-1989
;       APPLICATION NUMBER: 87,002
;       FILING DATE: 18-AUG-1987
;       APPLICATION NUMBER: 8,810
;       FILING DATE: 30-JAN-1987
        APPLICATION NUMBER: 948,376
        FILING DATE: 31-DEC-1986
        APPLICATION NUMBER: 932,193
;       FILING DATE: 17-NOV-1986
;SEQ ID NO:18:
;       LENGTH: 144
5187153-18


  Query Match             25.8%;  Score 244.5;  DB 5;  Length 144;
  Best Local Similarity   31.8%;  Pred. No. 1.5e-18;
  Matches   47;  Conservative   15;  Mismatches   47;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |      |::|| |  :|: | |||| || ||::|::|||: | ||
Db      24 DSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRTVAA-- 81

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                          |    : |||||    | ||  :
Db      82 -----------------------------------CNLPVIRGPCRAFIQLWAFDAVK 104

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     105 GKCVLFPYGGCQGNGNKFYSEKECREYC 132


RESULT   9
US-08-358-160-72
; Sequence 72, Application US/08358160
; Patent No. 5663143
;  GENERAL INFORMATION:
;    APPLICANT:  LEY, Arthur C.
;    APPLICANT:  LADNER, Robert C.
;    APPLICANT:  GUTERMAN, Sonia K.
;    APPLICANT:  ROBERTS, Bruce L.
;    APPLICANT:  MARKLAND, William
;    APPLICANT:  KENT, Rachel B.
;    TITLE OF INVENTION:  ENGINEERED HUMAN-DERIVED KUNITZ
;    TITLE OF INVENTION:  DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
;    NUMBER OF SEQUENCES:  234
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W. Suite 300
;      CITY:  Washington
;      STATE:  District of Columbia
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,160
;      FILING DATE:  16-DEC-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/133,031
;      FILING DATE:  13-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/009,319
;      FILING DATE:  26-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/664,989
;      FILING DATE:  01-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/487,063
;      FILING DATE:  02-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/240,160
;      FILING DATE:  02-SEP-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cooper, Iver P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  LEY=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248638
;  INFORMATION FOR SEQ ID NO:  72:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  147 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-358-160-72


  Query Match             25.8%;  Score 244.5;  DB 1;  Length 147;
  Best Local Similarity   32.4%;  Pred. No. 1.6e-18;
  Matches   48;  Conservative   14;  Mismatches   47;  Indels   39;  Gaps

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           | | :    | |      |::|| |  :|: | |||| || ||::|::|||: | ||
Db      24 DSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRTVAA-- 81

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
```

```
                                                |    | |||||    | ||  :
Db      82 ----------------------------------CNLPIVRGPCRAFIQLWAFDAVK 104

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||:|| | : ||: |   |
Db     105 GKCVLFPYGGCQGNGNKFYSEKECREYC 132


RESULT  10
5466783-24
;Patent No. 5466783
;    APPLICANT: Wun, Tze-Chein,;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
;    TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
;    NUMBER OF SEQUENCES: 26
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/93,285
;      FILING DATE: 15-JUL-1993
     PRIOR APPLICATION DATA:
       APPLICATION NUMBER: 566,280
       FILING DATE: 13-AUG-1990
;      APPLICATION NUMBER: 123,753
;      FILING DATE: 23-NOV-1987
;      APPLICATION NUMBER: 77,366
;      FILING DATE: 23-JUL-1987
;SEQ ID NO:24:
;      LENGTH: 127
5466783-24


  Query Match             25.7%;  Score 243.5;  DB 5;  Length 127;
  Best Local Similarity   32.7%;  Pred. No. 1.7e-18;
  Matches   48;  Conservative   14;  Mismatches   46;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
             | | :    | |     |::|| |  :|: | |||| || ||::|::|||: | ||
Db       3 DSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRTVAA-- 60

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                |    | |||||    | ||  :
Db      61 ----------------------------------CNLPIVRGPCRAFIQLWAFDAVK 83

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLR 155
             |  | ||||:|| | : ||: |  |
Db      84 GKCVLFPYGGCQGNGNKFYSEKECECR 110


RESULT  11
5466783-21
;Patent No. 5466783
;    APPLICANT: Wun, Tze-Chein,;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
;    TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
;    NUMBER OF SEQUENCES: 26
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/93,285
;      FILING DATE: 15-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 566,280
;      FILING DATE: 13-AUG-1990
;      APPLICATION NUMBER: 123,753
;      FILING DATE: 23-NOV-1987
;      APPLICATION NUMBER: 77,366
;      FILING DATE: 23-JUL-1987
;SEQ ID NO:21:
;      LENGTH: 123
5466783-21


  Query Match             25.5%;  Score 241.5;  DB 5;  Length 123;
  Best Local Similarity   31.8%;  Pred. No. 2.6e-18;
  Matches   47;  Conservative   15;  Mismatches   47;  Indels   39;  Gaps    1;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
             | | :    | |    : |::|| |  :|: | |||| || ||: :::|||: | ||
Db       3 DSCQLDHAQGPCLGMISRYFYNGTSMACETFQYGGCLGNGNNFASQKECLQTCRTVAA-- 60

Qy      69 TGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVER 128
                                                |    | |||||    | ||  :
Db      61 ----------------------------------CNLPIVQGPCRAFIRLWAFDAAQ 83

Qy     129 NSCNNFIYGGCRGNKNSYRSEEACMLRC 156
             |  | ||||||| | : |:: |   |
Db      84 GKCVLFTYGGCRGNGNKFYSQKECKEYC 111


RESULT  12
5223482-22
;Patent No. 5223482
;    APPLICANT: SCHILLING, JAMES W.;PONTE, PHYLLIS A.;CORDELL,
;BARBARA
;    TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
;INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
;    NUMBER OF SEQUENCES: 34
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/361,912
;      FILING DATE: 06-JUN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 359,911
;      FILING DATE: 12-MAY-1989
;      APPLICATION NUMBER: 87,002
;      FILING DATE: 18-AUG-1987
;      APPLICATION NUMBER: 8,810
;      FILING DATE: 30-JAN-1987
;      APPLICATION NUMBER: 948,376
;      FILING DATE: 31-DEC-1986
;      APPLICATION NUMBER: 932,193
;      FILING DATE: 17-NOV-1986
;SEQ ID NO:22:
;      LENGTH: 122
5223482-22


  Query Match             24.6%;  Score 233.5;  DB 5;  Length 122;
  Best Local Similarity   33.6%;  Pred. No. 1.8e-17;
  Matches   44;  Conservative   15;  Mismatches   33;  Indels   39;  Gaps    1;

Qy      26 RWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENATGDLATSRNAADSSVPS 85
           |::|| |  :|: |:|||| || ||:|:::|||: | ||
Db      22 RYFYNGTSMACETFLYGGCMGNLNNFLSQKECLQTCRTV---------------------- 60

Qy      86 APRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNS 145
                        | |    | |||||    | ||  :  |  | ||||:|| |
Db      61 -----------------EACNLPIVQGPCRAFIQLWAFDAVKGKCVRFSYGGCKGNGNK 102

Qy     146 YRSEEACMLRC 156
           : |:: |   |
Db     103 FYSQKECKEYC 113


RESULT  13
US-07-828-920A-1
; Sequence 1, Application US/07828920A
; Patent No. 5312736
;  GENERAL INFORMATION:
;    APPLICANT:  Rasmussen, Jesper
;    APPLICANT:  No. 5312736dfang, Ole Juul
;    TITLE OF INVENTION:  Anticoagulant Protein
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 53127360 No. 5312736disk of No. 5312736th America, Inc
;      STREET:  405 Lexington Avenue, Suite 6200
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10174-6201
```

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/828,920A
;      FILING DATE:  19920127
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DK 4080/89
;      FILING DATE:  18-AUG-1989
;      APPLICATION NUMBER:  WO PCT/DK90/00212
;      FILING DATE:  17)AUG)1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zelson, Steve T.
;      REGISTRATION NUMBER:  30335
;      REFERENCE/DOCKET NUMBER:  3287.204-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;   INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  276 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..276
US-07-828-920A-1


  Query Match             24.6%;  Score 233.5;  DB 1;  Length 276;
  Best Local Similarity   33.6%;  Pred. No. 5.1e-17;
  Matches   51;  Conservative   26;  Mismatches   64;  Indels   11;  Gaps    3;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           ||| : :  | ||  : |::||     |: | |||| || ||: | |||   |    :
Db      95 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC---EDGP 151

Qy      69 TG----DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124
             |    :  |  || ::|:      | ::  |   |:   :|   |  | |||:  |:|:
Db     152 NGFQVDNYGTQLNAVNNSLTP----QSTKVPSLFEFHGPSWCLTPADRGLCRANENRFYY 207

Qy     125 DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           :     |  | | || ||:|:: |:: |:  |
Db     208 NSVIGKCRPFKYSGCGGNENNFTSKQECLRAC 239


RESULT  14
US-08-437-841-9
; Sequence 9, Application US/08437841
; Patent No. 5563123
;  GENERAL INFORMATION:
;    APPLICANT:  Innis, Michael
;    APPLICANT:  Creasey, Abla
;    TITLE OF INVENTION:  Chimeric Proteins
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton St.
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/437,841
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/286,521
;      FILING DATE:  05-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Savereide, Paul B.
;      REGISTRATION NUMBER:  36,914
;      REFERENCE/DOCKET NUMBER:  0990.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-601-2585
;      TELEFAX:  510-655-3542
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  276 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-437-841-9


  Query Match             24.6%;  Score 233.5;  DB 1;  Length 276;
  Best Local Similarity   33.6%;  Pred. No. 5.1e-17;
  Matches   51;  Conservative   26;  Mismatches   64;  Indels   11;  Gaps

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           ||| : :  | ||  : |::||     |: | |||| || ||: | |||   |    :
Db      95 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC---EDGP 151

Qy      69 TG----DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124
             |    :  |  || ::|:      | ::  |   |:   :|   |  | |||:  |:|:
Db     152 NGFQVDNYGTQLNAVNNSLTP----QSTKVPSLFEFHGPSWCLTPADRGLCRANENRFYY 207

Qy     125 DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           :     |  | | || ||:|:: |:: |:  |
Db     208 NSVIGKCRPFKYSGCGGNENNFTSKQECLRAC 239


RESULT  15
US-08-286-521-9
; Sequence 9, Application US/08286521
; Patent No. 5589359
;  GENERAL INFORMATION:
;    APPLICANT:  Innis, Michael
;    APPLICANT:  Creasey, Abla
;    TITLE OF INVENTION:  Chimeric Proteins
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton St.
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/286,521
;      FILING DATE:  05-AUG-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Savereide, Paul B.
;      REGISTRATION NUMBER:  36,914
;      REFERENCE/DOCKET NUMBER:  0990.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-601-2585
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;      TELEFAX:  510-655-3542
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  276 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-286-521-9


  Query Match             24.6%;  Score 233.5;  DB 1;  Length 276;
  Best Local Similarity   33.6%;  Pred. No. 5.1e-17;
  Matches   51;  Conservative   26;  Mismatches   64;  Indels   11;  Gaps    3;

Qy       9 DFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENA 68
           ||| : :  | ||  : |::||     |: | |||| || ||: | |||   |    :
Db      95 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC---EDGP 151

Qy      69 TG----DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYF 124
           |    :  |  || ::|:      | ::  |   |:   :|   |  | |||:  |:|:
Db     152 NGFQVDNYGTQLNAVNNSLTP----QSTKVPSLFEFHGPSWCLTPADRGLCRANENRFYY 207

Qy     125 DVERNSCNNFIYGGCRGNKNSYRSEEACMLRC 156
           :     |  | | || ||:|:: |:: |:  |
Db     208 NSVIGKCRPFKYSGCGGNENNFTSKQECLRAC 239


Search completed: January 31, 2001, 15:05:21
Job time: 113 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 31, 2001, 15:05:08 ; Search time 15.54 Seconds
(without alignments)
742.800 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 170
Sequence: 1 ADRERSIHDFCLVSKVVGRC.....ACMLRCFRQQENPPLPLGSK 170

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

[redacted]arched: 195891 seqs, 67900655 residues

[redacted]rd size : 0

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	7.6	252	2	JG0185	hepatocyte growth
2	11	6.5	302	1	TIRTGK	tissue factor path
3	9	5.3	58	1	TIHABK	isoinhibitor K (BP
4	9	5.3	65	1	TIVIVC	venom basic protei
5	8	4.7	922	2	T23573	hypothetical prote
6	8	4.7	973	2	S54534	coatomer complex b
7	8	4.7	1599	2	T16210	hypothetical prote
8	8	4.7	2844	2	S28291	hypothetical prote
9	7	4.1	57	1	TIFHBP	proteinase inhibit
10	7	4.1	61	1	TIHCBP	proteinase inhibit
11	7	4.1	62	2	S19327	venom basic protei
12	7	4.1	120	1	JQ1280	lipid transfer pro
13	7	4.1	125	1	TIHOBI	alpha-1-microglobu
14	7	4.1	183	2	T28711	hypothetical prote
15	7	4.1	210	2	S66484	insulin-like growt
16	7	4.1	253	2	S49183	hypothetical prote
17	7	4.1	438	2	T12494	hypothetical prote
18	7	4.1	500	2	F71978	hypothetical prote
19	7	4.1	507	2	H82378	probable long-chai
20	7	4.1	988	2	I50611	protein-tyrosine k
21	7	4.1	1663	1	C3HU	complement C3 prec
22	7	4.1	2167	2	T34395	hypothetical prote
23	7	4.1	2172	2	T20145	hypothetical prote
24	7	4.1	4660	2	T42737	gp330 protein prec
25	6	3.5	55	2	S30332	proteinase inhibit
26	6	3.5	56	2	JN0380	trypsin inhibitor
27	6	3.5	57	1	TIRIV2	venom basic protei
28	6	3.5	57	1	TINJVC	venom basic protei
29	6	3.5	57	2	S13846	venom animal Kunit
30	6	3.5	57	2	A59204	basic proteinase i
31	6	3.5	58	2	S10063	isoaprotinin G2 -
32	6	3.5	59	2	S00371	isoaprotinin G1 -
33	6	3.5	60	1	TIBOR	serum basic protei
34	6	3.5	60	2	D81898	hypothetical prote
35	6	3.5	61	1	TIVIT1	venom basic protei
36	6	3.5	62	2	S07451	proteinase inhibit
37	6	3.5	62	2	S01802	chymotrypsin inhib
38	6	3.5	62	2	S01803	chymotrypsin inhib
39	6	3.5	62	2	A44180	taicatoxin serine
40	6	3.5	63	1	TIFFAF	acrosin inhibitor
41	6	3.5	63	1	TIMTC3	chymotrypsin inhib
42	6	3.5	76	1	WMVZR0	9K protein - vacci
43	6	3.5	76	2	S04855	Alzheimer's diseas
44	6	3.5	76	2	S03607	Alzheimer's diseas
45	6	3.5	76	2	S06678	Alzheimer's diseas

ALIGNMENTS

RESULT 1
JG0185
hepatocyte growth factor activator inhibitor type 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JG0185
R;Itoh, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Koono, M.
Biochem. Biophys. Res. Commun. 255, 740-748, 1999
A;Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first
A;Reference number: JG0185; MUID:99160423
A;Accession: JG0185
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-252 <ITO>
A;Cross-references: GB:AF099016
C;Superfamily: animal Kunitz-type proteinase inhibitor homology
F;133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 7.6%; Score 13; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 FIYGGCRGNKNSY 146
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Db 161 FIYGGCRGNKNSY 173

RESULT 2
TIRTGK
tissue factor pathway inhibitor precursor - rat
N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: JX0213
R;Enjyoji, K.; Emi, M.; Mukai, T.; Kato, H.
J. Biochem. 111, 681-687, 1992
A;Title: cDNA cloning and expression of rat tissue factor pathway
A;Reference number: JX0213; MUID:92348361
A;Accession: JX0213
A;Molecule type: mRNA
A;Residues: 1-302 <ENJ>
A;Cross-references: DDBJ:D10926; NID:g220916; PIDN:BAA01724.1; PID:g220917
A;Experimental source: liver
C;Comment: This serine proteinase inhibitor regulates clotting by factor Xa-de
C;Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor com
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase in
C;Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-302/Product: tissue factor pathway inhibitor #status predicted <MAT>
F;53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;124-174/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

F;222-272/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;288-291/Region: heparin binding #status predicted
F;53-103,62-86,78-99,124-174,133-157,149-170,222-272,231-255,247-268/Disulfide bonds: #s
F;63/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predict
F;134/Inhibitory site: Arg (coagulation factor X) #status predicted
F;144,251,261/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;232/Inhibitory site: Lys (unidentified proteinase) #status predicted

Query Match 6.5%; Score 11; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 FIYGGCRGNKN 144
||||||||||
Db 81 FIYGGCRGNKN 91

RESULT 3
TIHABK
Isoinhibitor K (BPI type) - Roman snail
C;Species: Helix pomatia (Roman snail)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 05-Aug-1994
C;Accession: A91232; A01225
R;Tschesche, H.; Dietl, T.
Eur. J. Biochem. 58, 439-451, 1975
A;Title: The amino-acid sequence of isoinhibitor K from snails (Helix pomatia). A sequen
A;Reference number: A91232; MUID:76043680
A;Accession: A91232
A;Molecule type: protein
A;Residues: 1-58 <TSC>
R;Dietl, T.; Tschesche, H.
Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976
A;Title: Die Disulfidbruecken des Trypsin-Kallikrein-Inhibitors K aus Weinbergschnecken
A;Reference number: A91666; MUID:76141310
A;Contents: annotation; disulfide bonds
C;Comment: This is one of several isoinhibitors of broad specificity that are secreted i
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: pyroglutamic acid; serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 5.3%; Score 9; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

134 FIYGGCRGN 142
|||||||||
35 FIYGGCRGN 43

RESULT 4
TIVIVC
venom basic proteinase inhibitor III - sand viper
N;Alternate names: venom chymotrypsin inhibitor
C;Species: Vipera ammodytes (sand viper)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Aug-1996
C;Accession: A01223
R;Ritonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 746, 138-145, 1983
A;Title: The primary structure Of Vipera ammodytes venom chymotrypsin inhibitor.
A;Reference number: A01223
A;Accession: A01223
A;Molecule type: protein
A;Residues: 1-65 <RIT>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor; venom
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;7-57,16-40,32-53/Disulfide bonds: #status predicted
F;17/Inhibitory site: Leu (chymotrypsin) #status predicted

Query Match 5.3%; Score 9; DB 1; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 FIYGGCRGN 142
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Db 35 FIYGGCRGN 43

RESULT 5
T23573
hypothetical protein K10D3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23573
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19762
A;Accession: T23573
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-922 <WIL>
A;Cross-references: EMBL:Z75545; PIDN:CAA99886.1; GSPDB:GN00019; CESP:K10D3.4
A;Experimental source: clone K10D3
C;Genetics:
A;Gene: CESP:K10D3.4
A;Map position: 1
A;Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 4.7%; Score 8; DB 2; Length 922;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 GCDGNSNN 50
||||||||
Db 552 GCDGNSNN 559

RESULT 6
S54534
coatomer complex beta chain - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YD8419.05c; protein YDR238c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 29-Sep-1999
C;Accession: S54534; A55123; C55123; S50260
R;Oliver, K.; Harris, D.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54530
A;Accession: S54534
A;Molecule type: DNA
A;Residues: 1-973 <OLI>
A;Cross-references: EMBL:Z49701; NID:g817819; PIDN:CAA89724.1; PID:g817824; MIPS:YDR
A;Experimental source: strain AB972
R;Duden, R.; Hosobuchi, M.; Hamamoto, S.; Winey, M.; Byers, B.; Schekman, R.
J. Biol. Chem. 269, 24486-24495, 1994
A;Title: Yeast beta- and beta'-coat proteins (COP). Two coatomer subunits essenti
A;Reference number: A55123; MUID:95014199
A;Accession: A55123
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-411,'E',413-973 <DUD>
A;Cross-references: GB:U11236; NID:g595412; PIDN:AAA61710.1; PID:g595413
A;Accession: C55123
A;Molecule type: protein
A;Residues: 353-362;496-514;645-655;934-942 <DU2>
C;Genetics:
A;Gene: SGD:SEC26
A;Cross-references: SGD:S0002646; MIPS:YDR238c
A;Map position: 4R
C;Superfamily: coatomer complex beta chain
C;Keywords: blocked amino end; transmembrane protein

F;391-407/Domain: transmembrane #status predicted <TM1>
F;409-425/Domain: transmembrane #status predicted <TM2>
F;587-603/Domain: transmembrane #status predicted <TM3>

Query Match 4.7%; Score 8; DB 2; Length 973;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 DLATSRNA 78
||||||||
Db 347 DLATSRNA 354

RESULT 7
T16210
hypothetical protein F30H5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16210
A;Pauley, A.; Stellyes, L.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F30H5.
A;Reference number: Z18478
A;Accession: T16210
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1599 <PAU>
A;Cross-references: EMBL:U29096; NID:g861390; PID:g861393; PIDN:AAA68408.1; CESP:F30H5.3
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F30H5.3
A;Introns: 12/1; 59/2; 85/3; 124/3; 217/2; 534/3; 560/1; 1549/1

Query Match 4.7%; Score 8; DB 2; Length 1599;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 GCDGNSNN 50
||||||||
Db 704 GCDGNSNN 711

RESULT 8
S28291
hypothetical protein ZC84.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Aug-1997
C;Accession: S28291
R;Thomas, K.
submitted to the EMBL Data Library, December 1992
A;Reference number: S28285
A;Accession: S28291
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2844 <THO>
A;Cross-references: EMBL:Z19157
C;Genetics:
A;Introns: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12
493/1; 2555/1; 2720/1; 2739/3; 2819/1
C;Superfamily: animal Kunitz-type proteinase inhibitor homology
F;220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>
F;343-395/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
F;442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>
F;546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BPI4>
F;654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPI5>
F;1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BPI6>
F;1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BPI7>
F;1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BPI8>
F;1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BPI9>
F;2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BPI10>

Query Match 4.7%; Score 8; DB 2; Length 2844;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 GCDGNSNN 50
||||||||
Db 580 GCDGNSNN 587

RESULT 9
TIFHBP
proteinase inhibitor - flesh fly (Sarcophaga bullata)
C;Species: Sarcophaga bullata
C;Date: 07-Feb-1992 #sequence_revision 22-Jul-1994 #text_change 07-May-1999
C;Accession: A37294
R;Papayannopoulos, I.A.; Biemann, K.
Protein Sci. 1, 278-288, 1992
A;Title: Amino acid sequence of a protease inhibitor isolated from Sarcophaga
A;Reference number: A37294; MUID:93284121
A;Accession: A37294
A;Molecule type: protein
A;Residues: 1-57 <PAP>
A;Experimental source: hemolymph
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase
C;Keywords: serine proteinase inhibitor
F;6-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;6-56,15-39,31-52/Disulfide bonds: #status predicted
F;16/Inhibitory site: Arg (chymotrypsin) #status predicted

Query Match 4.1%; Score 7; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 136 YGGCRGN 142
|||||||
Db 36 YGGCRGN 42

RESULT 10
TIHCBP
proteinase inhibitor (BPI-type) - horseshoe crab (Tachypleus tridentatus)
C;Species: Tachypleus tridentatus
C;Date: 08-Mar-1989 #sequence_revision 22-Jul-1994 #text_change 24-Feb-1995
C;Accession: A26923
R;Nakamura, T.; Hirai, T.; Tokunaga, F.; Kawabata, S.; Iwanaga, S.
J. Biochem. 101, 1297-1306, 1987
A;Title: Purification and amino acid sequence of Kunitz-type protease inhibitor found
A;Reference number: A26923; MUID:88007472
A;Accession: A26923
A;Molecule type: protein
A;Residues: 1-61 <NAK>
A;Experimental source: hemocytes
C;Comment: The inhibitory activity is similar to bovine basic proteinase inhibitor.
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor ho
C;Keywords: serine proteinase inhibitor
F;8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;8-58,17-41,33-54/Disulfide bonds: #status predicted
F;18/Inhibitory site: Arg (chymotrypsin, elastase, trypsin, plasmin, plasma kallikrei

Query Match 4.1%; Score 7; DB 1; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 VTGPCRA 117
|||||||
Db 13 VTGPCRA 19

RESULT 11
S19327

venom basic proteinase inhibitor - leaf-nosed viper
N;Alternate names: trypsin inhibitor (Kunitz-type)
C;Species: Eristocophis macmahoni (leaf-nosed viper)
C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
C;Accession: S19327
R;Siddiqi, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991
A;Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Leaf-
A;Reference number: S19327; MUID:92077130
A;Accession: S19327
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-62 <SID>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor; venom
F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>

Query Match 4.1%; Score 7; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 NFIYGGC 139
|||||||
Db 29 NFIYGGC 35

RESULT 12
JQ1280
lipid transfer protein EP2 precursor - carrot
N;Alternate names: extracellular protein 2
C;Species: Daucus carota (carrot)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JQ1280
R;Sterk, P.; Booij, H.; Schellekens, G.A.; Van Kammen, A.; De Vries, S.C.
Plant Cell 3, 907-921, 1991
A;Title: Cell-specific expression of the carrot EP2 lipid transfer protein gene.
A;Reference number: JQ1280; MUID:92361243
A;Accession: JQ1280
A;Molecule type: mRNA
A;Residues: 1-120 <STE>
A;Cross-references: GB:M64746; NID:g167553; PIDN:AAB96834.1; PID:g167554
C;Comment: This protein locates in cell walls.
C;Comment: The gene encoding for this protein is expressed in the embryogenic cell cultu
C;Superfamily: phospholipid transfer protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-120/Product: lipid transfer protein EP2 #status predicted <LIP>

Query Match 4.1%; Score 7; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 TANAVTG 113
|||||||
Db 83 TANAVTG 89

RESULT 13
TIHOBI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
N;Alternate names: EI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI
C;Species: Equus caballus (domestic horse)
C;Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 05-May-2000
C;Accession: A01210; A45653
R;Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A;Reference number: A90685; MUID:85225967
A;Accession: A01210
A;Molecule type: protein
A;Residues: 3-125 <HOC>
R;Veeraragavan, K.; Singh, K.; Wachter, E.; Hochstrasser, K.
Biochem. Int. 26, 405-413, 1992
A;Title: Characterization of a trypsin inhibitor from equine urine.
A;Reference number: A45653; MUID:92328813
A;Accession: A45653
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12,'E',14-33 <VEE>
A;Cross-references: PIDN:AAB22430.1; PID:g250858
A;Experimental source: urine
A;Note: sequence extracted from NCBI backbone (NCBIP:107966)
C;Comment: This inhibitory fragment, released from native ITI after limited proteolys
first domain interacts weakly with PMN-granulocytic elastase and not at all with panc
C;Comment: The amino acid at position P2' (19-Met) appears to determine the specifici
d elastase; those with leucine interact strongly.
C;Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocali
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
F;17/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F;26/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;73/Inhibitory site: Arg (trypsin) #status predicted

Query Match 4.1%; Score 7; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 YGGCRGN 142
|||||||
Db 93 YGGCRGN 99

RESULT 14
T28711
hypothetical protein T21D12.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28711
R;Woessner, J.
submitted to the EMBL Data Library, August 1997
A;Description: The sequence of C. elegans cosmid T21D12.
A;Reference number: Z20514
A;Accession: T28711
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-183 <WOE>
A;Cross-references: EMBL:AF016687; PIDN:AAC48097.1; GSPDB:GN00022; CESP:T21D12.12
A;Experimental source: strain Bristol N2; clone T21D12
C;Genetics:
A;Gene: CESP:T21D12.12
A;Map position: 4
A;Introns: 57/3; 88/1; 126/1; 147/2

Query Match 4.1%; Score 7; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 GCDGNSN 49
|||||||
Db 58 GCDGNSN 64

RESULT 15
S66484
insulin-like growth factor II precursor - spiny dogfish
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: S66484; S58053
R;Duguay, S.J.; Chan, S.J.; Mommsen, T.P.; Steiner, D.F.
FEBS Lett. 371, 69-72, 1995
A;Title: Divergence of insulin-like growth factors I and II in the elasmobranch

A;Reference number: S66484; MUID:95394151
A;Accession: S66484
A;Molecule type: mRNA
A;Residues: 1-210 <DUG>
A;Cross-references: EMBL:Z50082; NID:g902732; PIDN:CAA90413.1; PID:g902733
A;Experimental source: liver
C;Superfamily: insulin
C;Keywords: growth factor
F;1-49/Domain: signal sequence #status predicted <SIG>
F;50-210/Product: insulin-like growth factor II #status predicted <MAT>
F;50-82/Domain: insulin chain B-like #status predicted <DOB>
F;83-90/Domain: insulin connecting peptide C-like #status predicted <CPE>
F;91-111/Domain: insulin chain A-like #status predicted <DOA>
F;112-117/Domain: peptide D #status predicted <DOD>
F;118-210/Domain: carboxyl-terminal propeptide (E peptide) #status predicted <CHE>
F;58-97,70-110,96-101/Disulfide bonds: #status predicted

Query Match 4.1%; Score 7; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      13 VSKVVGR 19
           |||||||
Db      78 VSKVVGR 84
```

Search completed: January 31, 2001, 15:07:08
Job time: 120 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 31, 2001, 15:05:52 ; Search time 10.05 Seconds
(without alignments)
546.268 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 170
Sequence: 1 ADRERSIHDFCLVSKVVGRC.....ACMLRCFRQQENPPLPLGSK 170

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 88757 seqs, 32294092 residues

Word size : 0

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11	6.5	302	1	TFPI_RAT	Q02445 rattus norv
2	9	5.3	58	1	ISIK_HELPO	P00994 helix pomat
3	9	5.3	65	1	IVB3_VIPAA	P00992 vipera ammo
4	8	4.7	973	1	COPB_YEAST	P41810 saccharomyc
5	8	4.7	1416	1	YN81_CAEEL	Q03610 caenorhabdi
6	7	4.1	57	1	SBPI_SARBU	P26228 sarcophaga
7	7	4.1	61	1	IBPI_TACTR	P16044 tachypleus
8	7	4.1	62	1	IVBT_ERIMA	P24541 eristocophi
9	7	4.1	120	1	NLTP_DAUCA	P27631 daucus caro
10	7	4.1	123	1	IATR_HORSE	P04365 equus cabal
11	7	4.1	521	1	TRPE_BUCAI	Q44695 buchnera ap
12	7	4.1	1663	1	CO3_HUMAN	P01024 homo sapien
13	7	4.1	4660	1	LRP2_RAT	P98158 rattus norv
14	6	3.5	52	1	ISP2_GALME	P81906 galleria me
15	6	3.5	55	1	ISH1_STOHE	P31713 stoichactis
16	6	3.5	55	1	ISH2_STOHE	P81129 stoichactis
17	6	3.5	56	1	ITR4_RADMA	P16344 radianthus
18	6	3.5	57	1	IVB2_HEMHA	P00985 hemachatus
19	6	3.5	57	1	IVB2_NAJNI	P00986 naja nivea
20	6	3.5	57	1	IVBT_NAJNA	P20229 naja naja (
21	6	3.5	60	1	IBPS_BOVIN	P00975 bos taurus
22	6	3.5	61	1	ITRS_RAT	P19603 rattus norv
23	6	3.5	61	1	IVB1_VIPAA	P00991 vipera ammo
24	6	3.5	62	1	IP52_ANESU	P10280 anemonia su
25	6	3.5	62	1	ISC1_BOMMO	P10831 bombyx mori
26	6	3.5	62	1	ISC2_BOMMO	P10832 bombyx mori
27	6	3.5	63	1	ICS3_BOMMO	P07481 bombyx mori
28	6	3.5	63	1	IMAP_DROFU	P11424 drosophila
29	6	3.5	69	1	CRPT_BOOMI	P81162 boophilus m
30	6	3.5	76	1	A4_MACMU	P29216 macaca mula
31	6	3.5	76	1	Y8K9_VACCV	P07608 vaccinia vi
32	6	3.5	87	1	A4_MACFA	P53601 macaca fasc
33	6	3.5	94	1	S110_RAT	P05943 rattus norv
34	6	3.5	100	1	BPT1_BOVIN	P00974 bos taurus
35	6	3.5	100	1	BPT2_BOVIN	P04815 bos taurus
36	6	3.5	110	1	IBP_CARCR	P00993 caretta car
37	6	3.5	115	1	YDG5_SCHPO	Q10493 schizosacch
38	6	3.5	122	1	UPTI_PIG	Q29100 sus scrofa
39	6	3.5	123	1	IATR_SHEEP	P13371 ovis aries
40	6	3.5	145	1	RL13_STACA	Q00990 staphyloco
41	6	3.5	150	1	RL15_MYCGE	P47415 mycoplasma
42	6	3.5	160	1	Y964_MYCTU	P71546 mycobacteri
43	6	3.5	162	1	YLR2_EBV	P03197 epstein-bar
44	6	3.5	176	1	RL1X_HUMAN	Q02543 homo sapien
45	6	3.5	176	1	RL1X_RAT	P11249 rattus norv

ALIGNMENTS

RESULT 1
TFPI_RAT
ID TFPI_RAT STANDARD; PRT; 302 AA.
AC Q02445;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR (TFPI) (LIPOPROTEIN-
DE ASSOCIATED COAGULATION INHIBITOR) (LACI) (EXTRINSIC PATHWAY INHIBITOR)
DE (EPI).
GN TFPI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=92348361; PubMed=1639767;
RA Enjyoji K.-I., Emi M., Mukai T., Kato H.;
RT "cDNA cloning and expression of rat tissue factor pathway inhibitor
RT (TFPI).";
RL J. Biochem. 111:681-687(1992).
CC -!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC LIPOPROTEINS IN PLASMA.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN HEART, LUNG, KIDNEY, AND
CC AORTIC ENDOTHELIAL CELLS.
CC -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
CC HIGHLY SIMILAR TO TFP2.
CC ---

CC ---
DR EMBL; D10926; BAA01724.1; -.
DR PIR; JX0213; TIRTGK.
DR HSSP; P10646; 1TFX.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW Signal.
FT SIGNAL 1 28
FT CHAIN 29 302 TISSUE FACTOR PATHWAY INHIBITOR.
FT DOMAIN 53 103 BPTI/KUNITZ INHIBITOR 1
FT (VII(A)/TISSUE FACTOR BINDING SITE).
FT DOMAIN 124 174 BPTI/KUNITZ INHIBITOR 2

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FT                                     (FACTOR X(A) BINDING SITE).
FT   DOMAIN      222    272        BPTI/KUNITZ INHIBITOR 3.
FT   DISULFID     53    103        BY SIMILARITY.
FT   DISULFID     62     86        BY SIMILARITY.
FT   DISULFID     78     99        BY SIMILARITY.
FT   ACT_SITE     63     64        REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    124    174        BY SIMILARITY.
FT   DISULFID    133    157        BY SIMILARITY.
FT   DISULFID    149    170        BY SIMILARITY.
FT   ACT_SITE    134    135        REACTIVE BOND (BY SIMILARITY).
FT   DISULFID    222    272        BY SIMILARITY.
FT   DISULFID    231    255        BY SIMILARITY.
FT   DISULFID    247    268        BY SIMILARITY.
FT   ACT_SITE    232    233        REACTIVE BOND (BY SIMILARITY).
FT   CARBOHYD    144    144        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    251    251        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    261    261        N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   302 AA;  34554 MW;  F9AE82130A24A59F CRC64;

  Query Match             6.5%;  Score 11;  DB 1;  Length 302;
  Best Local Similarity   100.0%;  Pred. No. 0.00035;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    134 FIYGGCRGNKN 144
          ||||||||||| 
Db     81 FIYGGCRGNKN 91


RESULT   2
ISIK_HELPO
ID   ISIK_HELPO     STANDARD;      PRT;    58 AA.
AC   P00994;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-AUG-1990 (Rel. 15, Last annotation update)
DE   ISOINHIBITOR K.
OS   Helix pomatia (Roman snail) (Edible snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Helicoidea; Helicidae; Helix.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76043680; PubMed=1183446;
RA   Tschesche H., Dietl T.;
RT   "The amino-acid sequence of isoinhibitor K form snails (Helix
RT   pomatia). A sequence determination by automated Edman degradation and
RT   mass-spectral identification of the phenylthiohydantoins.";
RL   Eur. J. Biochem. 58:439-451(1975).
     [2]
     DISULFIDE BONDS.
     MEDLINE=76141310; PubMed=3462;
RA   Dietl T., Tschesche H.;
RT   "The disulfide bridges of the trypsin-kallikrein inhibitor K from
RT   snails (Helix pomatia). Thermal inactivation and proteolysis by
RT   thermolysin.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:139-145(1976).
CC   -!- FUNCTION: THIS IS ONE OF SEVERAL ISOINHIBITORS OF BROAD
CC       SPECIFICITY THAT ARE SECRETED INTO THE MUCUS OF THE SNAIL.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   PIR; A01225; TIHABK.
DR   HSSP; P00974; 1BRB.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Serine protease inhibitor.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID      7     57
FT   DISULFID     16     40
FT   DISULFID     32     53
FT   ACT_SITE     17     18       REACTIVE BOND (BY SIMILARITY).
SQ   SEQUENCE   58 AA;  6451 MW;  6796586C488453B7 CRC64;

  Query Match             5.3%;  Score 9;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    134 FIYGGCRGN 142
          ||||||||| 
Db     35 FIYGGCRGN 43


RESULT   3
IVB3_VIPAA
ID   IVB3_VIPAA     STANDARD;      PRT;    65 AA.
AC   P00992;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-MAY-1992 (Rel. 22, Last annotation update)
DE   VENOM BASIC PROTEASE INHIBITOR III (VENOM CHYMOTRYPSIN INHIBITOR).
OS   Vipera ammodytes ammodytes (Western sand viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Vipera.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=VENOM;
RA   Ritonja A., Meloun B., Gubensek F.;
RT   "The primary structure of Vipera ammodytes venom chymotrypsin
RT   inhibitor.";
RL   Biochim. Biophys. Acta 746:138-145(1983).
CC   -!- FUNCTION: THIS PROTEIN INHIBITS CHYMOTRYPSIN.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   PIR; A01223; TIVIVC.
DR   HSSP; P31713; 1SHP.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Venom; Serine protease inhibitor.
FT   DISULFID      7     57
FT   DISULFID     16     40
FT   DISULFID     32     53
FT   ACT_SITE     17     18       REACTIVE BOND (BY SIMILARITY).
SQ   SEQUENCE   65 AA;  7556 MW;  9D526F8E3BF7CC57 CRC64;

  Query Match             5.3%;  Score 9;  DB 1;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    134 FIYGGCRGN 142
          ||||||||| 
Db     35 FIYGGCRGN 43


RESULT   4
COPB_YEAST
ID   COPB_YEAST     STANDARD;      PRT;    973 AA.
AC   P41810; Q03779;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).
GN   SEC26 OR YDR238C OR YD8419.05C.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC   Saccharomycetaceae; Saccharomyces.
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=RSY255;
RX   MEDLINE=95014199; PubMed=7929113;
RA   Duden R., Hosobuchi M., Hamamoto S., Winey M., Byers B., Schekman R.;
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RT   "Yeast beta- and beta'-coat proteins (COP). Two coatomer subunits
RT   essential for endoplasmic reticulum-to-Golgi protein traffic.";
RL   J. Biol. Chem. 269:24486-24495(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RA   Oliver K., Harris D., Barrell B.G., Rajandream M.A.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
CC       TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CC       CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
CC       PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
CC       NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
CC       MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
CC       TRANSPORT OF DILYSINE-TAGGED PROTEINS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
CC       BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
CC       ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
CC       VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
CC   -!- PTM: THE N-TERMINUS IS BLOCKED.
CC   -!- MISCELLANEOUS: BREFELDIN A INDUCES DISSOCIATION FROM THE GOLGI OF
CC       THE BETA-COP AND PRESUMABLY THE OTHER COATOMER SUBUNITS (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: SIGNIFICANT, OF THE N-TERMINAL HALF OF BETA-COP WITH
CC       THOSE OF BETA-ADAPTINS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U11236; AAA61710.1; -.
DR   EMBL; Z49701; CAA89724.1; -.
DR   SGD; S0002646; SEC26.
KW   Transport; Protein transport; Golgi stack; Membrane; Phosphorylation.
FT   CONFLICT    412    412       D -> E (IN REF. 1).
SQ   SEQUENCE   973 AA;  109019 MW;  885420DB026BCFA3 CRC64;


  Query Match             4.7%;  Score 8;  DB 1;  Length 973;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      71 DLATSRNA 78
           ||||||||
Db     347 DLATSRNA 354


RESULT   5
YN81_CAEEL
ID   YN81_CAEEL     STANDARD;      PRT;  1416 AA.
AC   Q03610;
DT   01-FEB-1994 (Rel. 28, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   HYPOTHETICAL 316.1 KDA PROTEIN ZC84.1 IN CHROMOSOME III.
GN   ZC84.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=94150718; PubMed=7906398;
RA   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA   Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA   Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA   Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA   Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
RA   Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA   Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA   Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
RA   Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA   Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA   Wohldman P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C
RT   elegans.";
RL   Nature 368:32-38(1994).
RN   [2]
RP   REVISIONS.
RC   STRAIN=BRISTOL N2;
RA   Jones S.J.M.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: STRONG, TO D1044.3.
CC   -!- SIMILARITY: CONTAINS 5 PROTEASE INHIBITOR DOMAINS BELONGING TO THE
CC       BPTI/KUNITZ FAMILY OF INHIBITORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z19157; CAA79569.1; -.
DR   PIR; S28291; S28291.
DR   HSSP; P07204; 2ADX.
DR   WORMPEP; ZC84.1; CE15020.
DR   INTERPRO; IPR000561; -.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR002899; -.
DR   PFAM; PF01683; EB; 3.
DR   PFAM; PF00014; Kunitz_BPTI; 5.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 5.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
KW   Hypothetical protein; Serine protease inhibitor; Repeat.
FT   DOMAIN      212    266       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      352    387       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      434    484       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      538    590       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      646    698       BPTI/KUNITZ INHIBITOR.
SQ   SEQUENCE   1416 AA;  152986 MW;  531CACE1CB22F70D CRC64;


  Query Match             4.7%;  Score 8;  DB 1;  Length 1416;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      43 GCDGNSNN 50
           ||||||||
Db     572 GCDGNSNN 579


RESULT   6
SBPI_SARBU
ID   SBPI_SARBU     STANDARD;      PRT;    57 AA.
AC   P26228;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   PROTEASE INHIBITOR (SBPI).
OS   Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Oestroidea; Sarcophagidae; Sarcophaga.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=LARVAL HEMOLYMPH;
RX   MEDLINE=93284121; PubMed=1304909;
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RA   Papayannopoulos I.A., Biemann K.;
RT   "Amino acid sequence of a protease inhibitor isolated from Sarcophaga
RT   bullata determined by mass spectrometry.";
RL   Protein Sci. 1:278-288(1992).
CC   -!- FUNCTION: SEEMS TO INHIBITS TRYPSIN.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   PIR; A37294; A37294.
DR   HSSP; P10646; 1ADZ.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Serine protease inhibitor.
FT   DISULFID      6     56       BY SIMILARITY.
FT   DISULFID     15     39       BY SIMILARITY.
FT   DISULFID     31     52       BY SIMILARITY.
FT   ACT_SITE     16     17       REACTIVE BOND (TRYPSIN) (BY SIMILARITY).
SQ   SEQUENCE   57 AA;  6518 MW;  FC512C5399E87241 CRC64;


  Query Match             4.1%;  Score 7;  DB 1;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    136 YGGCRGN 142
          |||||||
Db     36 YGGCRGN 42


RESULT   7
IBPI_TACTR
ID   IBPI_TACTR     STANDARD;      PRT;    61 AA.
AC   P16044;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   01-AUG-1990 (Rel. 15, Last annotation update)
DE   PROTEINASE INHIBITOR (BPI-TYPE).
OS   Tachypleus tridentatus (Japanese horseshoe crab).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC   Limulidae; Tachypleus.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=HEMOCYTE;
RX   MEDLINE=88007472; PubMed=3308864;
RA   Nakamura T., Hirai T., Tokunaga F., Kawabata S., Iwanaga S.;
RT   "Purification and amino acid sequence of Kunitz-type protease
RT   inhibitor found in the hemocytes of horseshoe crab (Tachypleus
RT   tridentatus).";
RL   J. Biochem. 101:1297-1306(1987).
CC   -!- FUNCTION: INHIBITOR OF TRYPSIN AND CHYMOTRYPSIN.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   PIR; A26923; A26923.
DR   HSSP; P00974; 4TPI.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Serine protease inhibitor.
FT   DISULFID      8     58       BY SIMILARITY.
FT   DISULFID     17     41       BY SIMILARITY.
FT   DISULFID     33     54       BY SIMILARITY.
FT   ACT_SITE     18     19       REACTIVE BOND (BY SIMILARITY).
SQ   SEQUENCE   61 AA;  6825 MW;  730E82CDD0653E48 CRC64;


  Query Match             4.1%;  Score 7;  DB 1;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    111 VTGPCRA 117
          |||||||
Db     13 VTGPCRA 19


RESULT   8
IVBT_ERIMA
ID   IVBT_ERIMA     STANDARD;      PRT;    62 AA.
AC   P24541;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   01-MAY-1992 (Rel. 22, Last annotation update)
DE   VENOM TRYPSIN INHIBITOR.
OS   Eristocophis macmahoni (Leaf-nosed viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Eristocophis.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=VENOM;
RX   MEDLINE=92077130; PubMed=1743283;
RA   Siddiqi A.R., Zaidi Z.H., Joernvall H.;
RT   "Purification and characterization of a Kunitz-type trypsin inhibitor
RT   from Leaf-nosed viper venom.";
RL   FEBS Lett. 294:141-143(1991).
CC   -!- FUNCTION: THIS PROTEIN INHIBITS TRYPSIN AND KALLIKREIN.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   PIR; S19327; S19327.
DR   HSSP; P31713; 1SHP.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Venom; Serine protease inhibitor.
FT   DISULFID      2     52       BY SIMILARITY.
FT   DISULFID     11     35       BY SIMILARITY.
FT   DISULFID     27     48       BY SIMILARITY.
FT   ACT_SITE     12     13       REACTIVE BOND (BY SIMILARITY).
SQ   SEQUENCE   62 AA;  6772 MW;  0A2ED0ADB20DF938 CRC64;


  Query Match             4.1%;  Score 7;  DB 1;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    133 NFIYGGC 139
          |||||||
Db     29 NFIYGGC 35


RESULT   9
NLTP_DAUCA
ID   NLTP_DAUCA     STANDARD;      PRT;   120 AA.
AC   P27631;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (EXTRACELLULAR
DE   PROTEIN 2).
GN   EP2.
OS   Daucus carota (Carrot).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
OC   euasterids II; Apiales; Apiaceae; Daucus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NORTHRUP KING;
RX   MEDLINE=92361243; PubMed=1822991;
RA   Sterk P., Booij H., Schellekens G.A., van Kammen A., de Vries S.C.;
RT   "Cell-specific expression of the carrot EP2 lipid transfer protein
RT   gene.";
RL   Plant Cell 3:907-921(1991).
CC   -!- FUNCTION: PLANT NONSPECIFIC LIPID-TRANSFER PROTEINS TRANSFER
CC       PHOSPHOLIPIDS AS WELL AS GALACTOLIPIDS ACROSS MEMBRANES. MAY PLAY
CC       A ROLE IN WAX OR CUTIN DEPOSITION IN THE CELL WALLS OF EXPANDING
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CC       EPIDERMAL CELLS AND CERTAIN SECRETORY TISSUES.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN PROTODERM CELLS OF SOMATIC AND
CC       ZYGOTIC EMBRYOS, AND TRANSIENTLY EXPRESSED IN EPIDERMAL CELL
CC       LAYERS OF LEAVES, FLOWERS, AND SEEDS.
CC   -!- SIMILARITY: BELONGS TO THE PLANT LTP FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M64746; AAB96834.1; -.
DR   PIR; JQ1280; JQ1280.
DR   HSSP; P19656; 1AFH.
DR   INTERPRO; IPR000528; -.
DR   PFAM; PF00279; LTP; 1.
DR   PRINTS; PR00382; LIPIDTRNSFER.
DR   PROSITE; PS00597; PLANT_LTP; 1.
KW   Lipid-binding; Transport; Signal.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    120       NONSPECIFIC LIPID-TRANSFER PROTEIN.
FT   DISULFID     30     79       BY SIMILARITY.
FT   DISULFID     40     56       BY SIMILARITY.
FT   DISULFID     57    102       BY SIMILARITY.
FT   DISULFID     77    116       BY SIMILARITY.
SQ   SEQUENCE   120 AA;  12504 MW;  E85C6EBA5E592214 CRC64;


  Query Match             4.1%;  Score 7;  DB 1;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     107 TANAVTG 113
           |||||||
Db      83 TANAVTG 89


RESULT  10
IATR_HORSE
ID   IATR_HORSE     STANDARD;      PRT;   123 AA.
AC   P04365;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   01-APR-1990 (Rel. 14, Last annotation update)
DE   INTER-ALPHA-TRYPSIN INHIBITOR (ITI) (HI-14) (INHIBITORY FRAGMENT OF
DE   ITI) (FRAGMENT).
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=85225967; PubMed=2408637;
RA   Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
RT   "Kunitz-type proteinase inhibitors derived by limited proteolysis of
RT   the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
RT   trypsin-released inhibitors from horse and pig inter-alpha-trypsin
RT   inhibitors.";
RL   Biol. Chem. Hoppe-Seyler 366:473-478(1985).
CC   -!- FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER
CC       LIMITED PROTEOLYSIS WITH TRYPSIN, CONTAINS TWO HOMOLOGOUS DOMAINS.
CC       WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPSIN, THE
CC       FIRST DOMAIN INTERACTS WEAKLY WITH PMN-GRANULOCYTIC ELASTASE AND
CC       NOT AT ALL WITH PANCREATIC ELASTASE.
CC   -!- MISCELLANEOUS: THE AMINO ACID AT POSITION P2' (17) APPEARS TO
CC       DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN I.
CC       INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH
CC       CHYMOTRYPSIN AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   PIR; A01210; TIHOBI.
DR   HSSP; P10646; 1ADZ.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW   Plasma; Glycoprotein; Serine protease inhibitor; Repeat.
FT   NON_TER       1      1
FT   DOMAIN        1     56       I.
FT   DOMAIN       57    123       II.
FT   DISULFID      5     55
FT   DISULFID     14     38
FT   DISULFID     30     51
FT   DISULFID     61    111
FT   DISULFID     70     94
FT   DISULFID     86    107
FT   ACT_SITE     15     16       INHIBITORY SITE (P1) (CHYMOTRYPSIN,
FT                                ELASTASE).
FT   ACT_SITE     71     72       INHIBITORY SITE (P1) (TRYPSIN).
FT   CARBOHYD     24     24       N-LINKED (GLCNAC. . .).
FT   NON_TER     123    123
SQ   SEQUENCE   123 AA;  13510 MW;  CE1A9120774411D5 CRC64;


  Query Match             4.1%;  Score 7;  DB 1;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     136 YGGCRGN 142
           |||||||
Db      91 YGGCRGN 97


RESULT  11
TRPE_BUCAI
ID   TRPE_BUCAI     STANDARD;      PRT;   521 AA.
AC   Q44695;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN   TRPE OR BUPT01.
OS   Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS   symbiotic bacterium).
OG   Plasmid pBAp.
OC   Bacteria; Proteobacteria; gamma subdivision; Buchnera.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96215866; PubMed=8642610;
RA   Rouhbakhsh D., Lai C.-Y., von Dohlen C.D., Clark M.A., Baumann L.,
RA   Baumann P., Moran N.A., Voegtlin D.J.;
RT   "The tryptophan biosynthetic pathway of aphid endosymbionts
RT   (Buchnera): genetics and evolution of plasmid-associated anthranilate
RT   synthase (trpEG) within the aphididae.";
RL   J. Mol. Evol. 42:414-421(1996).
CC   -!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
CC       PYRUVATE + L-GLUTAMATE.
CC   -!- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC   -!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
CC       SIMILARITY).
CC   -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC       USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC       GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L43555; AAD09346.1; -.
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DR   PFAM; PF00425; chorismate_bind; 1.
DR   PRINTS; PR00095; ANTSNTHASEI.
KW   Tryptophan biosynthesis; Lyase; Plasmid.
SQ   SEQUENCE   521 AA;  58695 MW;  28B5F8FEE7DF4271 CRC64;


  Query Match             4.1%;  Score 7;  DB 1;  Length 521;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 LVSKVVG 18
           |||||||
Db     400 LVSKVVG 406


RESULT  12
CO3_HUMAN
ID   CO3_HUMAN      STANDARD;      PRT;  1663 AA.
AC   P01024;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN].
GN   C3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85140166; PubMed=2579379;
RA   de Bruijn M.H.L., Fey G.H.;
RT   "Human complement component C3: cDNA coding sequence and derived
RT   primary structure.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:708-712(1985).
RN   [2]
RP   SEQUENCE OF 672-748.
RX   MEDLINE=76069169; PubMed=1238393;
RA   Hugli T.E.;
RT   "Human anaphylatoxin (C3a) from the third component of complement.
RT   Primary structure.";
RL   J. Biol. Chem. 250:8293-8301(1975).
RN   [3]
RP   SEQUENCE OF 1409-1563.
RX   MEDLINE=88154452; PubMed=3279119;
RA   Daoudaki M.E., Becherer J.D., Lambris J.D.;
RT   "A 34-amino acid peptide of the third component of complement
RT   mediates properdin binding.";
RL   J. Immunol. 140:1577-1580(1988).
RN   [4]
RP   SEQUENCE OF 988-1036.
RX   MEDLINE=82174534; PubMed=6175959;
RA   Thomas M.L., Janatova J., Gray W.R., Tack B.F.;
RT   "Third component of human complement: localization of the internal
RT   thiolester bond.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:1054-1058(1982).
RN   [5]
RP   STRUCTURE BY NMR OF C3A.
RX   MEDLINE=88276894; PubMed=3260670;
RA   Nettesheim D.G., Edalji R.P., Mollison K.W., Greer J., Zuiderweg E.R.;
RT   "Secondary structure of complement component C3a anaphylatoxin in
RT   solution as determined by NMR spectroscopy: differences between
RT   crystal and solution conformations.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:5036-5040(1988).
RN   [6]
RP   MUTAGENESIS OF THIOESTER BOND REGION.
RX   MEDLINE=92250565; PubMed=1577777;
RA   Isaac L., Isenman D.E.;
RT   "Structural requirements for thioester bond formation in human
RT   complement component C3. Reassessment of the role of thioester bond
RT   integrity on the conformation of C3.";
RL   J. Biol. Chem. 267:10062-10069(1992).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=93106233; PubMed=8416818;
RA   Dolmer K., Sottrup-Jensen L.;
RT   "Disulfide bridges in human complement component C3b.";
RL   FEBS Lett. 315:85-90(1993).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 996-1303.
RX   MEDLINE=98259089; PubMed=9596584;
RA   Nagar B., Jones R.G., Diefenbach R.J., Isenman D.E., Rini J.M.;
RT   "X-ray crystal structure of C3d: a C3 fragment and ligand for
RT   complement receptor 2.";
RL   Science 280:1277-1281(1998).
RN   [9]
RP   VARIANT C3F/S.
RX   MEDLINE=89309808; PubMed=2473125;
RA   Poznansky M.C., Clissold P.M., Lachmann P.J.;
RT   "The difference between human C3F and C3S results from a single amino
RT   acid change from an asparagine to an aspartate residue at position
RT   1216 on the alpha-chain of the complement component, C3.";
RL   J. Immunol. 143:1254-1258(1989).
RN   [10]
RP   ERRATUM (RETRACTION OF ABOVE ARTICLE).
RX   MEDLINE=90063087; PubMed=2584723;
RA   Poznansky M.C., Clissold P.M., Lachmann P.J.;
RL   J. Immunol. 143:3860-3862(1989).
RN   [11]
RP   VARIANTS GLY-102 AND PRO-314.
RX   MEDLINE=91011240; PubMed=1976733;
RA   Botto M., Yong Fong K., So A.K., Koch C., Walport M.J.;
RT   "Molecular basis of polymorphisms of human complement component C3.";
RL   J. Exp. Med. 172:1011-1017(1990).
RN   [12]
RP   VARIANT ASN-549.
RX   MEDLINE=95050640; PubMed=7961791;
RA   Singer L., Whitehead W.T., Akama H., Katz Y., Fishelson Z.,
RA   Wetsel R.A.;
RT   "Inherited human complement C3 deficiency. An amino acid substitution
RT   in the beta-chain (ASP549 to ASN) impairs C3 secretion.";
RL   J. Biol. Chem. 269:28494-28499(1994).
RN   [13]
RP   VARIANT GLN-1320.
RA   Watanabe Y., Matsui N., Yan K., Nishimukai H., Tokunaga K.,
RA   Juji T., Kobayashi N., Kohsaka T.;
RT   "A novel C3 allotype C3'F02'has an amino acid substitution that may
RT   inhibit iC3b synthesis and cause C3-hypocomplementemia.";
RL   Mol. Immunol. 30:62-62(1993).
CC   -!- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
CC       COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL
CC       REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS.
CC       AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE
CC       THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.
CC   -!- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3,
CC       C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC       INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC       PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC       BASOPHILIC LEUKOCYTES.
CC   -!- SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG
CC       RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
CC       BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN,
CC       RELEASING C3A ANAPHYLATOXIN & GENERATING C3B (BETA CHAIN + ALPHA'
CC       CHAIN).
CC   -!- POLYMORPHISM: THERE ARE TWO ALLELES: C3S (C3 SLOW), THE MOST
CC       COMMON ALLELE IN ALL RACES AND C3F (C3 FAST), RELATIVELY FREQUENT
CC       IN CAUCASOIDS, LESS COMMON IN BLACK AMERICAN, EXTREMELY RARE IN
CC       ORIENTALS.
CC   -!- DISEASE: C3 DEFICIENCY CAUSES A SUSCEPTIBILITY TO PYOGENIC
CC       INFECTION.
CC   -!- MISCELLANEOUS: C3B IS RAPIDLY SPLIT IN TWO POSITIONS BY FACTOR I
CC       AND A COFACTOR TO FORM IC3B (INACTIVATED C3B) AND C3F WHICH IS
CC       RELEASED.
CC   -!- MISCELLANEOUS: IC3B IS THE SLOWLY CLEAVED (POSSIBLY BY FACTOR I)
CC       TO FORM C3C AND C3DG. OTHER PROTEASES PRODUCE OTHER FRAGMENTS SUCH
CC       AS C3D OR C3G.
CC   -!- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
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CC   -!- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; K02765; AAA85332.1; -.
DR   PIR; A01257; C3HU.
DR   PIR; A27603; A27603.
DR   PDB; 1C3D; 18-NOV-98.
DR   SWISS-2DPAGE; P01024; HUMAN.
DR   MIM; 120700; -.
DR   INTERPRO; IPR000020; -.
DR   INTERPRO; IPR001134; -.
DR   INTERPRO; IPR001599; -.
DR   INTERPRO; IPR001840; -.
DR   INTERPRO; IPR002890; -.
DR   PFAM; PF00207; A2M; 1.
DR   PFAM; PF01835; A2M_N; 1.
DR   PFAM; PF01821; ANATO; 1.
DR   PFAM; PF01759; NTR; 1.
DR   PRINTS; PR00004; ANAPHYLATOXN.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW   Complement pathway; Complement alternate pathway; Plasma;
KW   Inflammatory response; Glycoprotein; Signal; Polymorphism;
KW   Disease mutation; 3D-structure.
FT   SIGNAL       1     22
FT   CHAIN       23   1663       COMPLEMENT C3.
FT   CHAIN       23    667       COMPLEMENT C3, BETA CHAIN.
FT   CHAIN      672   1663       COMPLEMENT C3, ALPHA CHAIN.
FT   PEPTIDE    672    748       C3A ANAPHYLATOXIN.
FT   CHAIN      749   1663       C3B ALPHA' CHAIN.
FT   PEPTIDE    749    954       C3C FRAGMENT.
FT   PEPTIDE    955   1303       C3DG FRAGMENT.
FT   PEPTIDE    955   1001       C3G FRAGMENT.
FT   PEPTIDE   1002   1303       C3D FRAGMENT.
FT   PEPTIDE   1304   1320       C3F FRAGMENT.
FT   SITE       748    749       CLEAVAGE (BY C3 CONVERTASE).
FT   SITE       954    955       CLEAVAGE (BY FACTOR I) (POTENTIAL).
FT   SITE      1303   1304       CLEAVAGE (BY FACTOR I).
FT   SITE      1320   1321       CLEAVAGE (BY FACTOR I).
FT   DOMAIN     693    728       ANAPHYLATOXIN-LIKE.
FT   DOMAIN    1424   1456       PROPERDIN-BINDING.
FT   DISULFID   559    816       INTERCHAIN.
FT   DISULFID   627    662
FT   DISULFID   693    720
FT   DISULFID   694    727
FT   DISULFID   707    728
FT   DISULFID   873   1513
FT   DISULFID  1101   1158
FT   DISULFID  1358   1489
FT   DISULFID  1389   1458
FT   DISULFID  1506   1511
FT   DISULFID  1518   1590
FT   DISULFID  1537   1661
FT   DISULFID  1637   1646
FT   CARBOHYD    85     85       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   939    939       N-LINKED (GLCNAC. . .).
FT   CARBOHYD  1617   1617       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   THIOLEST  1010   1013
FT   VARIANT    102    102       R -> G (IN ALLELE C3F).
FT                               /FTId=VAR_001983.
FT   VARIANT    314    314       L -> P.
FT                               /FTId=VAR_001984.
FT   VARIANT    549    549       D -> N (IN C3 DEFICIENCY; IMPAIRS

  Query Match             4.1%;  Score 7;  DB 1;  Length 1663;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps

Qy      46 GNSNNYL 52
           |||||||
Db     450 GNSNNYL 456


RESULT  13
LRP2_RAT
ID   LRP2_RAT       STANDARD;      PRT;  4660 AA.
AC   P98158;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN)
DE   (GLYCOPROTEIN 330).
GN   LRP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom...
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra...
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
RX   MEDLINE=95024033; PubMed=7937880;
RA   Saito A., Pietromonaco S., Loo A.K.C., Farquhar M.G.;
RT   "Complete cloning and sequencing of rat gp330/'megalin,' a
RT   distinctive member of the low density lipoprotein receptor gene
RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=95386696; PubMed=7544804;
RA   Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.E.,
RA   Norris K., Gliemann J., Christensen E.I.;
RT   "Evidence that epithelial glycoprotein 330/megalin mediates uptake of
RT   polybasic drugs.";
RL   J. Clin. Invest. 96:1404-1413(1995).
RN   [3]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=94172242; PubMed=7510321;
RA   Zheng G., Bachinsky D.R., Stamenkovic I., Strickland D.K., Brown D.,
RA   Andres G., McCluskey R.T.;
RT   "Organ distribution in rats of two members of the low-density
RT   lipoprotein receptor gene family, gp330 and LRP/alpa 2MR, and the
RT   receptor-associated protein (RAP).";
RL   J. Histochem. Cytochem. 42:531-542(1994).
CC   -!- FUNCTION: BINDS PLASMINOGEN, EXTRACELLULAR MATRIX COMPONENTS,
CC       PLASMINOGEN ACTIVATOR-PLASMINOGEN ACTIVATOR INHIBITOR TYPE I
CC       COMPLEX, APOLIPOPROTEIN E-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,
CC       LACTOFERRIN; CLUSTERIN AND CALCIUM.
CC   -!- FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLYBASIC DRUGS SUCH AS
CC       APROTININ, AMINOGLYCOSIDES AND POLYMYXIN B.
CC   -!- SUBUNIT: FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-
CC       ASSOCIATED PROTEIN (RAP).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXPRESSED IN
CC       CLATHRIN-COATED PITS; A SOLUBLE FORM IS POSSIBLY DERIVED BY
CC       CLEAVAGE AT THE CELL SURFACE.
CC   -!- TISSUE SPECIFICITY: EPITHELIAL CELLS OF KIDNEY GLOMERULUS AND
CC       PROXIMAL TUBULE, LUNG, EPIDIDYMIS, YOLK SAC, AMONG OTHERS.
CC   -!- SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A DOMAINS.
CC   -!- SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.
CC   -!- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 3 SH3-BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 SH2-BINDING DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
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CC   ---------------------------------------------------------------------
DR   EMBL; L34049; AAA51369.1; -.
DR   HSSP; P01130; 1AJJ.
DR   INTERPRO; IPR000033; -.
DR   INTERPRO; IPR000152; -.
DR   INTERPRO; IPR000561; -.
DR   INTERPRO; IPR001881; -.
DR   INTERPRO; IPR002172; -.
DR   PFAM; PF00057; ldl_recept_a; 36.
DR   PFAM; PF00058; ldl_recept_b; 33.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   PROSITE; PS00010; ASX_HYDROXYL; 4.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 8.
DR   PROSITE; PS01187; EGF_CA; 3.
DR   PROSITE; PS01209; LDLRA_1; 31.
DR   PROSITE; PS50068; LDLRA_2; 36.
KW   Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane;
KW   Receptor; EGF-like domain; Signal.
FT   SIGNAL       1     25       POTENTIAL.
FT   CHAIN       26   4660       LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
FT                                PROTEIN 2.
FT   DOMAIN      26   4425       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM  4426   4446       POTENTIAL.
FT   DOMAIN    4447   4660       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      26     64       LDL-RECEPTOR CLASS A 1.
FT   DOMAIN      65    105       LDL-RECEPTOR CLASS A 2.
FT   DOMAIN     106    144       LDL-RECEPTOR CLASS A 3.
FT   DOMAIN     145    181       LDL-RECEPTOR CLASS A 4.
FT   DOMAIN     181    219       LDL-RECEPTOR CLASS A 5.
FT   DOMAIN     220    258       LDL-RECEPTOR CLASS A 6.
FT   DOMAIN     263    307       LDL-RECEPTOR CLASS A 7.
FT   DOMAIN     308    346       EGF-LIKE 1.
FT   DOMAIN     347    385       EGF-LIKE 2.
FT   DOMAIN     435    476       LDL-RECEPTOR CLASS B 1.
FT   DOMAIN     478    519       LDL-RECEPTOR CLASS B 2.
FT   DOMAIN     521    566       LDL-RECEPTOR CLASS B 3.
FT   DOMAIN     568    611       LDL-RECEPTOR CLASS B 4.
FT   DOMAIN     612    652       LDL-RECEPTOR CLASS B 5.
FT   DOMAIN     658    704       EGF-LIKE 3.
FT   DOMAIN     752    793       LDL-RECEPTOR CLASS B 6.
FT   DOMAIN     795    835       LDL-RECEPTOR CLASS B 7.
FT   DOMAIN     837    879       LDL-RECEPTOR CLASS B 8.
FT   DOMAIN     881    923       LDL-RECEPTOR CLASS B 9.
FT   DOMAIN     969   1013       EGF-LIKE 4.
FT   DOMAIN    1023   1061       LDL-RECEPTOR CLASS A 8.
FT   DOMAIN    1064   1103       LDL-RECEPTOR CLASS A 9.
FT   DOMAIN    1108   1146       LDL-RECEPTOR CLASS A 10.
FT   DOMAIN    1148   1186       LDL-RECEPTOR CLASS A 11.
FT   DOMAIN    1186   1225       LDL-RECEPTOR CLASS A 12.
FT   DOMAIN    1229   1269       LDL-RECEPTOR CLASS A 13.
FT   DOMAIN    1270   1308       LDL-RECEPTOR CLASS A 14.
FT   DOMAIN    1311   1351       LDL-RECEPTOR CLASS A 15.
FT   DOMAIN    1350   1390       EGF-LIKE 5.
FT   DOMAIN    1391   1430       EGF-LIKE 6; CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN    1479   1520       LDL-RECEPTOR CLASS B 10.
FT   DOMAIN    1522   1563       LDL-RECEPTOR CLASS B 11.
FT   DOMAIN    1567   1609       LDL-RECEPTOR CLASS B 12.
FT   DOMAIN    1611   1654       LDL-RECEPTOR CLASS B 13.
FT   DOMAIN    1656   1696       LDL-RECEPTOR CLASS B 14.
FT   DOMAIN    1701   1742       EGF-LIKE 7.
FT   DOMAIN    1791   1832       LDL-RECEPTOR CLASS B 15.
FT   DOMAIN    1834   1882       LDL-RECEPTOR CLASS B 16.
FT   DOMAIN    1884   1930       LDL-RECEPTOR CLASS B 17.
FT   DOMAIN    1932   1972       LDL-RECEPTOR CLASS B 18.
FT   DOMAIN    1973   2013       LDL-RECEPTOR CLASS B 19.
FT   DOMAIN    2019   2060       EGF-LIKE 8.
FT   DOMAIN    2108   2156       LDL-RECEPTOR CLASS B 20.
FT   DOMAIN    2158   2201       LDL-RECEPTOR CLASS B 21.
FT   DOMAIN    2203   2245       LDL-RECEPTOR CLASS B 22.
FT   DOMAIN    2247   2289       LDL-RECEPTOR CLASS B 23.
FT   DOMAIN    2291   2332       LDL-RECEPTOR CLASS B 24.
FT   DOMAIN    2343   2384       EGF-LIKE 9.
FT   DOMAIN    2432   2477       LDL-RECEPTOR CLASS B 25.
FT   DOMAIN    2479   2518       LDL-RECEPTOR CLASS B 26.
FT   DOMAIN    2520   2562       LDL-RECEPTOR CLASS B 27.
FT   DOMAIN    2564   2604       LDL-RECEPTOR CLASS B 28.
FT   DOMAIN    2605   2647       LDL-RECEPTOR CLASS B 29.
FT   DOMAIN    2652   2694       EGF-LIKE 10.
FT   DOMAIN    2699   2739       LDL-RECEPTOR CLASS A 16.
FT   DOMAIN    2740   2778       LDL-RECEPTOR CLASS A 17.
FT   DOMAIN    2779   2820       LDL-RECEPTOR CLASS A 18.
FT   DOMAIN    2821   2862       LDL-RECEPTOR CLASS A 19.
FT   DOMAIN    2863   2903       LDL-RECEPTOR CLASS A 20.
FT   DOMAIN    2906   2947       LDL-RECEPTOR CLASS A 21.
FT   DOMAIN    2948   2992       LDL-RECEPTOR CLASS A 22.
FT   DOMAIN    2993   3031       LDL-RECEPTOR CLASS A 23.
FT   DOMAIN    3032   3072       LDL-RECEPTOR CLASS A 24.
FT   DOMAIN    3075   3112       LDL-RECEPTOR CLASS A 25.
FT   DOMAIN    3113   3153       EGF-LIKE 11.
FT   DOMAIN    3154   3194       EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN    3241   3282       LDL-RECEPTOR CLASS B 30.
FT   DOMAIN    3284   3333       LDL-RECEPTOR CLASS B 31.
FT   DOMAIN    3335   3377       LDL-RECEPTOR CLASS B 32.
FT   DOMAIN    3379   3420       LDL-RECEPTOR CLASS B 33.
FT   DOMAIN    3421   3461       LDL-RECEPTOR CLASS B 34.
FT   DOMAIN    3467   3511       EGF-LIKE 13.
FT   DOMAIN    3512   3552       LDL-RECEPTOR CLASS A 26.
FT   DOMAIN    3553   3593       LDL-RECEPTOR CLASS A 27.
FT   DOMAIN    3594   3634       LDL-RECEPTOR CLASS A 28.
FT   DOMAIN    3635   3675       LDL-RECEPTOR CLASS A 29.
FT   DOMAIN    3678   3718       LDL-RECEPTOR CLASS A 30.
FT   DOMAIN    3719   3758       LDL-RECEPTOR CLASS A 31.
FT   DOMAIN    3759   3797       LDL-RECEPTOR CLASS A 32.
FT   DOMAIN    3798   3836       LDL-RECEPTOR CLASS A 33.
FT   DOMAIN    3842   3882       LDL-RECEPTOR CLASS A 34.
FT   DOMAIN    3883   3924       LDL-RECEPTOR CLASS A 35.
FT   DOMAIN    3928   3966       LDL-RECEPTOR CLASS A 36.
FT   DOMAIN    3968   4008       EGF-LIKE 14.
FT   DOMAIN    4009   4050       EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN    4156   4197       LDL-RECEPTOR CLASS B 35.
FT   DOMAIN    4199   4241       LDL-RECEPTOR CLASS B 36.
FT   DOMAIN    4244   4284       LDL-RECEPTOR CLASS B 37.
FT   DOMAIN    4332   4370       EGF-LIKE 16.
FT   DOMAIN    4379   4413       EGF-LIKE 17.
FT   DOMAIN    4454   4460       SH3-BINDING (POTENTIAL).
FT   DOMAIN    4457   4463       SH3-BINDING (POTENTIAL).
FT   DOMAIN    4606   4609       SH2-BINDING (POTENTIAL).
FT   DOMAIN    4619   4625       SH3-BINDING (POTENTIAL).
FT   DOMAIN    4624   4630       SH3-BINDING (POTENTIAL).
FT   SITE      1743   1745       CELL ATTACHMENT SITE (POTENTIAL).
FT   DOMAIN    4522   4527       ENDOCYTOSIS SIGNAL (POTENTIAL).
FT   DOMAIN    4601   4606       ENDOCYTOSIS SIGNAL (POTENTIAL).
FT   DISULFID    28     40       BY SIMILARITY.
FT   DISULFID    35     53       BY SIMILARITY.
FT   DISULFID    47     62       BY SIMILARITY.
FT   DISULFID    67     80       BY SIMILARITY.
FT   DISULFID    74     93       BY SIMILARITY.
FT   DISULFID    87    103       BY SIMILARITY.
FT   DISULFID   108    120       BY SIMILARITY.
FT   DISULFID   115    133       BY SIMILARITY.
FT   DISULFID   127    142       BY SIMILARITY.
FT   DISULFID   147    157       BY SIMILARITY.
FT   DISULFID   152    170       BY SIMILARITY.
FT   DISULFID   164    179       BY SIMILARITY.
FT   DISULFID   183    195       BY SIMILARITY.
FT   DISULFID   190    208       BY SIMILARITY.

  Query Match             4.1%;  Score 7;  DB 1;  Length 4660;
  Best Local Similarity   100.0%;  Pred. No. 79;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      76 RNAADSS 82
           |||||||
Db    2014 RNAADSS 2020
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RESULT  14
ISP2_GALME
ID   ISP2_GALME     STANDARD;      PRT;    52 AA.
AC   P81906;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   INDUCIBLE SERINE PROTEASE INHIBITOR 2 (ISPI-2) (FRAGMENT).
OS   Galleria mellonella (Wax moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Pyraloidea; Pyralidae; Galleriinae; Galleria.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=HEMOLYMPH;
RX   MEDLINE=20193629; PubMed=10727944;
RA   Froebius A.C., Kanost M.R., Goetz P., Vilcinskas A.;
RT   "Isolation and characterization of novel inducible serine protease
RT   inhibitors from larval hemolymph of the greater wax moth Galleria
RT   mellonella.";
RL   Eur. J. Biochem. 267:2046-2053(2000).
CC   -!- FUNCTION: INHIBITS TRYPSIN AND THE TOXIN PROTEASE PR2 OF M.
CC       ANISOPLIAE. DOES NOT INHIBIT CHYMOTRYPSIN, SUBTILISIN CARLSBERG,
CC       PROTEINASE K, PORCINE PANCREATIC ELASTASE AND THE TOXIN PROTEASE
CC       PR1 OF M. ANISOPLIAE.
CC   -!- DEVELOPMENTAL STAGE: LAST INSTAR LARVAE.
CC   -!- INDUCTION: BY INFECTION.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Serine protease inhibitor.
FT   DISULFID     14     38       BY SIMILARITY.
FT   DISULFID     30     51       BY SIMILARITY.
FT   ACT_SITE     15     16       REACTIVE BOND (BY SIMILARITY).
FT   NON_TER      52     52
SQ   SEQUENCE   52 AA;  6057 MW;  31CED34D59C42ABE CRC64;

  Query Match             3.5%;  Score 6;  DB 1;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      39 FVYGGC 44
           ||||||
Db      33 FVYGGC 38


RESULT  15
ISH1_STOHE
ID   ISH1_STOHE     STANDARD;      PRT;    55 AA.
AC   P31713;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   KUNITZ-TYPE PROTEINASE INHIBITOR SHPI-1.
OS   Stoichactis helianthus (Carribean sea anemone) (Stichodactyla
OS   helianthus).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Stichodactylidae; Stichodactyla.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=97179757; PubMed=9027993;
RA   Delfin J., Martinez I., Antuch W., Morera V., Gonzalez Y.,
RA   Rodriguez R., Marquez M., Saroyan A., Larionova N., Diaz J.,
RA   Padron G., Chavez M.;
RT   "Purification, characterization and immobilization of proteinase
RT   inhibitors from Stichodactyla helianthus.";
RL   Toxicon 34:1367-1376(1996).
RN   [2]
RP   STRUCTURE BY NMR, AND DISULFIDE BONDS.
RX   MEDLINE=93215644; PubMed=8462542;
RA   Antuch W., Berndt K.D., Chavez M.A., Delfin J., Wuethrich K.;
RT   "The NMR solution structure of a Kunitz-type proteinase inhibitor
RT   from the sea anemone Stichodactyla helianthus.";
RL   Eur. J. Biochem. 212:675-684(1993).
CC   -!- FUNCTION: ACTIVE AGAINST SERINE, CYSTEINE, AND ASPARTIC
CC       PROTEINASES.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   PIR; S30332; S30332.
DR   PDB; 1SHP; 31-JAN-94.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Serine protease inhibitor; 3D-structure.
FT   DISULFID      3     53
FT   DISULFID     12     36
FT   DISULFID     28     49
FT   ACT_SITE     13     14       REACTIVE BOND (TRYPSIN).
FT   HELIX         2      4
FT   STRAND       17     22
FT   TURN         23     26
FT   STRAND       27     32
FT   TURN         36     37
FT   STRAND       43     43
FT   HELIX        46     53
SQ   SEQUENCE   55 AA;  6116 MW;  532B96E3127000D4 CRC64;

  Query Match             3.5%;  Score 6;  DB 1;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     134 FIYGGC 139
           ||||||
Db      31 FIYGGC 36


Search completed: January 31, 2001, 15:07:48
Job time: 116 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 31, 2001, 15:05:23 ; Search time 22.96 Seconds
(without alignments)
867.829 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 170
Sequence: 1 ADRERSIHDFCLVSKVVGRC.....ACMLRCFRQQENPPLPLGSK 170

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Word size : 0

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_15:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	100.0	252	4	O43291	O43291 homo sapien
2	170	100.0	252	4	O00271	O00271 homo sapien
3	144	84.7	252	4	O14895	O14895 homo sapien
4	13	7.6	195	11	Q9WU04	Q9wu04 mus musculu
5	13	7.6	252	11	Q9WU03	Q9wu03 mus musculu
6	9	5.3	58	5	Q9TWG0	Q9twg0 anemonia su
7	9	5.3	58	5	Q9TWF9	Q9twf9 anemonia su
8	8	4.7	59	5	Q9TWF8	Q9twf8 anemonia su
9	8	4.7	922	5	Q21418	Q21418 caenorhabdi
10	8	4.7	1195	5	Q9N343	Q9n343 caenorhabdi
11	8	4.7	1599	5	Q09983	Q09983 caenorhabdi
12	7	4.1	110	5	Q9VQU0	Q9vqu0 drosophila
13	7	4.1	183	5	O16784	O16784 caenorhabdi
14	7	4.1	210	13	Q91443	Q91443 squalus aca
15	7	4.1	230	13	O13000	O13000 xenopus lae
16	7	4.1	253	2	Q54224	Q54224 streptomyce
17	7	4.1	260	5	O46164	O46164 schistocerc
18	7	4.1	355	5	Q9VGQ8	Q9vgq8 drosophila
19	7	4.1	438	4	Q9Y4N9	Q9y4n9 homo sapien
20	7	4.1	499	2	Q9L2G7	Q9l2g7 streptomyce
21	7	4.1	500	2	Q9ZN02	Q9zn02 helicobacte
22	7	4.1	507	2	O87080	O87080 vibrio chol
23	7	4.1	514	5	Q9TWE5	Q9twe5 carcinoscor
24	7	4.1	521	2	Q9KGQ2	Q9kgq2 buchnera sp
25	7	4.1	653	5	Q9W3R0	Q9w3r0 drosophila
26	7	4.1	654	5	Q9VFX6	Q9vfx6 drosophila
27	7	4.1	719	5	Q9U021	Q9u021 giardia lam
28	7	4.1	719	5	Q9U019	Q9u019 giardia lam
29	7	4.1	763	5	Q9XZD0	Q9xzd0 drosophila
30	7	4.1	836	4	O94856	O94856 homo sapien
31	7	4.1	972	5	O44938	O44938 haemonchus
32	7	4.1	974	13	Q91735	Q91735 xenopus lae
33	7	4.1	988	13	Q07498	Q07498 gallus gall
34	7	4.1	1151	11	Q9QVN5	Q9qvn5 rattus sp.
35	7	4.1	1214	5	Q25338	Q25338 latrodectus
36	7	4.1	1474	5	O62504	O62504 caenorhabdi
37	7	4.1	1668	4	O15026	O15026 homo sapien
38	7	4.1	1787	10	Q9SJP0	Q9sjp0 arabidopsis
39	7	4.1	2167	5	O76840	O76840 caenorhabdi
40	7	4.1	2208	5	Q09515	Q09515 caenorhabdi
41	7	4.1	2230	5	Q9VAV4	Q9vav4 drosophila
42	7	4.1	2971	4	Q9Y5L9	Q9y5l9 homo sapien
43	7	4.1	3198	5	Q9U8G8	Q9u8g8 manduca sex
44	6	3.5	41	12	O11552	O11552 human
45	6	3.5	42	2	Q49201	Q49201 mycoplas

ALIGNMENTS

RESULT 1
O43291
ID O43291 PRELIMINARY; PRT; 252 AA.
AC O43291;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98010584; PubMed=9346890;
RA Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K.,
RA Kitamura N.;
RT "Purification and cloning of hepatocyte growth factor activator
RT inhibitor type 2, a Kunitz-type serine protease inhibitor.";
RL J. Biol. Chem. 272:27558-27564(1997).
DR EMBL; AB006534; BAA25024.1; -.
DR HSSP; P05067; 1TAW.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ; 2.
KW Serine protease inhibitor.
SQ SEQUENCE 252 AA; 28169 MW; F7D3D834ED631DF0 CRC64;

Query Match 100.0%; Score 170; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
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Db     28 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87

Qy     61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 147
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Qy    121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 197
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RESULT 2
O00271
ID O00271 PRELIMINARY; PRT; 252 AA.
AC O00271;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE BIKUNIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=97277372; PubMed=9115294;
RA Marlor C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M.,
RA Tamburini P.P.;
RT "Identification and cloning of human placental bikunin, a novel serine
RT protease inhibitor containing two Kunitz domains.";
RL J. Biol. Chem. 272:12202-12208(1997).
DR EMBL; U78095; AAC02781.1; -.
DR HSSP; P05067; 1TAW.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ; 2.
KW Serine protease inhibitor.
SQ SEQUENCE 252 AA; 28228 MW; A7D3360C0EECAB2B CRC64;

Query Match 100.0%; Score 170; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     28 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87

Qy     61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 147

Qy    121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 197
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RESULT 3
O14895
ID O14895 PRELIMINARY; PRT; 252 AA.
AC O14895;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE KUNITZ-TYPE PROTEASE INHIBITOR.
GN KOP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREATIC CANCER;
RA Mueller-Pillasch F., Wallrapp C., Bartels K., Varga G., Friess H.,
RA Buechler M., Adler G., Gress T.M.;
RL Biochim. Biophys. Acta 0:0-0(1997).
DR EMBL; AF027205; AAB84031.1; -.
DR HSSP; P05067; 1TAW.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ; 2.
KW Protease; Serine protease inhibitor.
SQ SEQUENCE 252 AA; 28231 MW; B21593466413841E CRC64;

Query Match 84.7%; Score 144; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 4.2e-150;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     27 WWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENATGDLATSRNAADSSVPSA 86
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     54 WWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENATGDLATSRNAADSSVPSA 113

Qy     87 PRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSY 146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    114 PRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSY 173

Qy    147 RSEEACMLRCFRQQENPPLPLGSK 170
          ||||||||||||||||||||||||
Db    174 RSEEACMLRCFRQQENPPLPLGSK 197
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RESULT 4
Q9WU04
ID Q9WU04 PRELIMINARY; PRT; 195 AA.
AC Q9WU04;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2 SPLICE VARIANT 1.
GN HAI2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=99160423; PubMed=10049781;
RA Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
RT "Hepatocyte growth factor activator inhibitor type 2 lacking the first
RT Kunitz-type serine proteinase inhibitor domain is a predominant
RT product in mouse but not in human.";
RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
DR EMBL; AF099019; AAD22173.1; -.
DR HSSP; P05067; 1TAW.
DR INTERPRO; IPR002223; -.
DR PFAM; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 195 AA; 21736 MW; EF49C83AB4E3EDE0 CRC64;

Query Match 7.6%; Score 13; DB 11; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    134 FIYGGCRGNKNSY 146
          |||||||||||||
Db    104 FIYGGCRGNKNSY 116
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RESULT 5
Q9WU03
ID Q9WU03 PRELIMINARY; PRT; 252 AA.
AC Q9WU03;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

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DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR TYPE 2.
GN   HAI2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=99160423; PubMed=10049781;
RA   Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
RT   "Hepatocyte growth factor activator inhibitor type 2 lacking the first
RT   Kunitz-type serine proteinase inhibitor domain is a predominant
RT   product in mouse but not in human.";
RL   Biochem. Biophys. Res. Commun. 255:740-748(1999).
DR   EMBL; AF099016; AAD22172.1; -.
DR   HSSP; P05067; 1TAW.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 2.
KW   Serine protease inhibitor.
SQ   SEQUENCE   252 AA;  27914 MW;  B2FF4B86924D4F8F CRC64;


  Query Match             7.6%;  Score 13;  DB 11;  Length 252;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    134 FIYGGCRGNKNSY 146
          |||||||||||||
Db    161 FIYGGCRGNKNSY 173


RESULT   6
Q9TWG0
ID   Q9TWG0      PRELIMINARY;      PRT;    58 AA.
AC   Q9TWG0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   KALICLUDINE 1, ASKC1.
OS   Anemonia sulcata (Snake-locks sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anemonia.
OX   NCBI_TaxID=6108;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96027617; PubMed=7559645;
RA   Schweitz H., Bruhn T., Guillemare E., Moinier D., Lancelin J.M.,
RA   Beress L., Lazdunski M.;
RT   "Kalicludines and kaliseptine. Two different classes of sea anemone
RT   toxins for voltage sensitive K+ channels.";
RL   J. Biol. Chem. 270:25121-25126(1995).
DR   HSSP; P10646; 1ADZ.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 1.
SQ   SEQUENCE   58 AA;  6691 MW;  253E068896B4BDCD CRC64;


  Query Match             5.3%;  Score 9;  DB 5;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.031;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    134 FIYGGCRGN 142
          |||||||||
Db     33 FIYGGCRGN 41


RESULT   7
Q9TWF9
ID   Q9TWF9      PRELIMINARY;      PRT;    58 AA.
AC   Q9TWF9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   KALICLUDINE 2, ASKC2.
OS   Anemonia sulcata (Snake-locks sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anemonia.
OX   NCBI_TaxID=6108;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96027617; PubMed=7559645;
RA   Schweitz H., Bruhn T., Guillemare E., Moinier D., Lancelin J.M.,
RA   Beress L., Lazdunski M.;
RT   "Kalicludines and kaliseptine. Two different classes of sea anemone
RT   toxins for voltage sensitive K+ channels.";
RL   J. Biol. Chem. 270:25121-25126(1995).
DR   HSSP; P12111; 2KNT.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 1.
SQ   SEQUENCE   58 AA;  6778 MW;  F102E71682F1A55C CRC64;


  Query Match             5.3%;  Score 9;  DB 5;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.031;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    134 FIYGGCRGN 142
          |||||||||
Db     33 FIYGGCRGN 41


RESULT   8
Q9TWF8
ID   Q9TWF8      PRELIMINARY;      PRT;    59 AA.
AC   Q9TWF8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   KALICLUDINE 3, ASKC3.
OS   Anemonia sulcata (Snake-locks sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anemonia.
OX   NCBI_TaxID=6108;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96027617; PubMed=7559645;
RA   Schweitz H., Bruhn T., Guillemare E., Moinier D., Lancelin J.M.,
RA   Beress L., Lazdunski M.;
RT   "Kalicludines and kaliseptine. Two different classes of sea anemone
RT   toxins for voltage sensitive K+ channels.";
RL   J. Biol. Chem. 270:25121-25126(1995).
DR   HSSP; P31713; 1SHP.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 1.
SQ   SEQUENCE   59 AA;  6738 MW;  0C7695C3F394D4A5 CRC64;


  Query Match             4.7%;  Score 8;  DB 5;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     15 KVVGRCRA 22
          ||||||||
Db      9 KVVGRCRA 16
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RESULT   9
Q21418
ID   Q21418      PRELIMINARY;      PRT;   922 AA.
AC   Q21418;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   K10D3.4 PROTEIN.
GN   K10D3.4.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mcmurray A.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94150718; PubMed=7906398;
RA   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA   Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA   Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA   Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA   Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA   Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA   Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA   Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA   Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
DR   EMBL; Z75545; CAA99886.1; -.
DR   HSSP; P10646; 1TFX.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR002899; -.
DR   PFAM; PF00014; Kunitz_BPTI; 5.
DR   PFAM; PF01683; EB; 1.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00280; BPTI_KUNITZ; 2.
KW   Serine protease inhibitor.
SQ   SEQUENCE   922 AA;  99995 MW;  0CCBBC0AE2524CFD CRC64;

  Query Match             4.7%;  Score 8;  DB 5;  Length 922;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      43 GCDGNSNN 50
           ||||||||
Db     552 GCDGNSNN 559


RESULT  10
Q9N343
ID   Q9N343      PRELIMINARY;      PRT;  1195 AA.
AC   Q9N343;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Y55F3BR.J PROTEIN.
GN   Y55F3BR.J.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC024830; AAF59608.1; -.
SQ   SEQUENCE   1195 AA;  131342 MW;  E77C3A6DF2272A18 CRC64;

  Query Match             4.7%;  Score 8;  DB 5;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      43 GCDGNSNN 50
           ||||||||
Db     887 GCDGNSNN 894


RESULT  11
Q09983
ID   Q09983      PRELIMINARY;      PRT;  1599 AA.
AC   Q09983;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   HYPOTHETICAL 171.7 KDA PROTEIN F30H5.3 IN CHROMOSOME III.
GN   F30H5.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Pauley A., Stellyes L.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: STRONG, TO C.ELEGANS ZC84.1.
CC   -!- SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
DR   EMBL; U29096; AAA68408.1; -.
DR   HSSP; P10646; 1TFX.
DR   WORMPEP; F30H5.3; CE01927.
DR   INTERPRO; IPR002198; -.
DR   INTERPRO; IPR002223; -.
DR   INTERPRO; IPR002899; -.
DR   PFAM; PF00014; Kunitz_BPTI; 6.
DR   PFAM; PF01683; EB; 3.
DR   PRINTS; PR00759; BASICPTASE.
DR   PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
DR   PROSITE; PS00280; BPTI_KUNITZ; 2.
KW   Hypothetical protein; Serine protease inhibitor.
FT   DOMAIN        7     10       POLY-LEU.
FT   DOMAIN     1520   1523       POLY-GLU.
SQ   SEQUENCE   1599 AA;  171658 MW;  AB5E6A1D86E9880D CRC64;

  Query Match             4.7%;  Score 8;  DB 5;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 6.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      43 GCDGNSNN 50
           ||||||||
Db     704 GCDGNSNN 711


RESULT  12
Q9VQU0
ID   Q9VQU0      PRELIMINARY;      PRT;   110 AA.
AC   Q9VQU0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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DE   CG10031 PROTEIN.
GN   CG10031.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003579; AAF51074.1; -.
DR   HSSP; P12111; 2KNT.
DR   FLYBASE; FBgn0031563; CG10031.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00759; BASICPTASE.
SQ   SEQUENCE   110 AA;  12240 MW;  BB3F2DF4A7EF509D CRC64;
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  Query Match             4.1%;  Score 7;  DB 5;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     136 YGGCRGN 142
           |||||||
Db      86 YGGCRGN 92
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RESULT  13
O16784
ID   O16784      PRELIMINARY;      PRT;   183 AA.
AC   O16784;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   SIMILAR TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
GN   T21D12.12.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=94150718; PubMed=7906398;
RA   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA   Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA   Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA   Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA   Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA   Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA   Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA   Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA   Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Woessner J.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF016687; AAC48097.1; -.
DR   HSSP; P10646; 1TFX.
DR   INTERPRO; IPR002223; -.
DR   PFAM; PF00014; Kunitz_BPTI; 2.
DR   PROSITE; PS00280; BPTI_KUNITZ; 1.
KW   Serine protease inhibitor.
SQ   SEQUENCE   183 AA;  20143 MW;  CCEE4BE2293CE32A CRC64;
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  Query Match             4.1%;  Score 7;  DB 5;  Length 183;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      43 GCDGNSN 49
           |||||||
Db      58 GCDGNSN 64
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RESULT  14
Q91443
ID   Q91443      PRELIMINARY;      PRT;   210 AA.
AC   Q91443;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   INSULIN-LIKE GROWTH FACTOR II PRECURSOR.
OS   Squalus acanthias (Spiny dogfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
OX   NCBI_TaxID=7797;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=95394151; PubMed=7545136;
RA   Duguay S.J., Chan S.J., Mommsen T.P., Steiner D.F.;
RT   "Divergence of insulin-like growth factors I and II in the
RT   elasmobranch, Squalus acanthias.";
RL   FEBS Lett. 371:59-72(1995).
CC   -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR   EMBL; Z50082; CAA90413.1; -.
DR   HSSP; P01344; 1GF2.
DR   INTERPRO; IPR000739; -.
DR   PFAM; PF00049; Insulin; 1.
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DR   PRINTS; PR00276; INSULINA.
DR   PRINTS; PR00277; INSULINB.
DR   PROSITE; PS00262; INSULIN; 1.
DR   PRODOM; PD001048; -; 1.
KW   Signal.
FT   SIGNAL        1     49       POTENTIAL.
FT   CHAIN        50    210       INSULIN-LIKE GROWTH FACTOR II.
SQ   SEQUENCE   210 AA;  23027 MW;  9B433B7C4749A03A CRC64;


  Query Match             4.1%;  Score 7;  DB 13;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 VSKVVGR 19
           |||||||
Db      78 VSKVVGR 84


RESULT  15
O13000
ID   O13000      PRELIMINARY;      PRT;   230 AA.
AC   O13000;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   PROTEASOME SUBUNIT Y (EC 3.4.99.46).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RA   Nonaka M., Namikawa C., Sasaki M., Salter-Cid L., Flajnik M.F.;
RL   J. Immunol. 0:0-0(0).
DR   EMBL; D87689; BAA19760.1; -.
DR   MEROPS; T01.010; -.
DR   INTERPRO; IPR000243; -.
DR   INTERPRO; IPR001353; -.
DR   PFAM; PF00227; proteasome; 1.
DR   PRINTS; PR00141; PROTEASOME.
DR   PROSITE; PS00854; PROTEASOME_B; 1.
KW   Proteasome; Hydrolase; Protease.
SQ   SEQUENCE   230 AA;  24553 MW;  2A1C9B3494473D87 CRC64;


  Query Match             4.1%;  Score 7;  DB 13;  Length 230;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      53 TKEECLK 59
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Db     178 TKEECLK 184


Search completed: January 31, 2001, 15:07:35
Job time: 132 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 31, 2001, 15:04:19 ; Search time 15.92 Seconds
(without alignments)
191.752 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 170
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 174772 seqs, 17957048 residues

Word size : 0

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	100.0	252	1	US-08-685-660A-7	Sequence 7, Appli
2	170	100.0	252	2	US-08-974-196-7	Sequence 7, Appli
3	26	15.3	26	1	US-08-685-660A-3	Sequence 3, Appli
4	26	15.3	26	2	US-08-974-196-3	Sequence 3, Appli
5	15	8.8	29	1	US-08-685-660A-2	Sequence 2, Appli
6	15	8.8	29	2	US-08-974-196-2	Sequence 2, Appli
7	10	5.9	15	1	US-08-685-660A-1	Sequence 1, Appli
8	10	5.9	15	2	US-08-974-196-1	Sequence 1, Appli
9	10	5.9	58	3	US-08-676-124-93	Sequence 93, Appl
10	10	5.9	58	3	US-08-676-124-103	Sequence 103, App
11	10	5.9	58	3	US-09-414-878-93	Sequence 93, Appl
12	10	5.9	58	3	US-09-414-878-103	Sequence 103, App
13	10	5.9	58	3	US-09-240-136-93	Sequence 93, Appl
14	10	5.9	58	3	US-09-240-136-103	Sequence 103, App
15	9	5.3	58	1	US-08-358-160-116	Sequence 116, App
16	9	5.3	58	3	US-08-676-124-111	Sequence 111, App
17	9	5.3	58	3	US-09-414-878-111	Sequence 111, App
18	9	5.3	58	3	US-09-240-136-111	Sequence 111, App
19	9	5.3	59	5	5466783-6	Patent No. 5466783
20	9	5.3	65	1	US-08-358-160-92	Sequence 92, Appl
21	9	5.3	65	5	5466783-12	Patent No. 5466783
22	8	4.7	58	1	US-08-463-155A-61	Sequence 61, Appl
23	8	4.7	58	1	US-08-463-432B-61	Sequence 61, Appl
24	8	4.7	58	3	US-08-676-124-96	Sequence 96, Appl
25	8	4.7	58	3	US-09-414-878-96	Sequence 96, Appl
26	8	4.7	58	3	US-09-240-136-96	Sequence 96, Appl
27	7	4.1	41	2	US-08-640-847C-41	Sequence 41, Appl
28	7	4.1	57	1	US-08-358-160-126	Sequence 126, App
29	7	4.1	57	2	US-08-829-876-152	Sequence 152, App
30	7	4.1	58	1	US-08-321-658B-4	Sequence 4, Appli
31	7	4.1	58	1	US-08-321-658B-5	Sequence 5, Appli
32	7	4.1	58	1	US-08-463-155A-1	Sequence 1, Appli
33	7	4.1	58	1	US-08-463-155A-2	Sequence 2, Appli
34	7	4.1	58	1	US-08-463-155A-3	Sequence 3, Appli
35	7	4.1	58	1	US-08-463-155A-4	Sequence 4, Appli
36	7	4.1	58	1	US-08-463-155A-45	Sequence 45, Appl
37	7	4.1	58	1	US-08-463-155A-46	Sequence 46, Appl
38	7	4.1	58	1	US-08-463-155A-47	Sequence 47, Appl
39	7	4.1	58	1	US-08-463-155A-48	Sequence 48, Appl
40	7	4.1	58	1	US-08-463-155A-49	Sequence 49, Appl
41	7	4.1	58	1	US-08-463-155A-50	Sequence 50, Appl
42	7	4.1	58	1	US-08-463-155A-51	Sequence 51, Appl
43	7	4.1	58	1	US-08-463-155A-52	Sequence 52, Appl
44	7	4.1	58	1	US-08-463-155A-53	Sequence 53, Appl
45	7	4.1	58	1	US-08-463-155A-54	Sequence 54, Appl

ALIGNMENTS

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RESULT 1
US-08-685-660A-7
; Sequence 7, Application US/08685660A
; Patent No. 5731412
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMOMURA, Takeshi
;    APPLICANT:  KAWAGUCHI, Toshiya
;    APPLICANT:  KITAMURA, Naomi
;    TITLE OF INVENTION:  NOVEL PROTEIN, DNA CODING FOR SAME
;    TITLE OF INVENTION:  AND METHOD OF PRODUCING THE PROTEIN
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/685,660A
;      FILING DATE:  24-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JPA Hei 7-187134
;      FILING DATE:  24-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  Q-42295
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-685-660A-7


  Query Match           100.0%;  Score 170;  DB 1;  Length 252;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-150;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
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Db      28 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 197


RESULT   2
US-08-974-196-7
; Sequence 7, Application US/08974196
; Patent No. 5854396
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMOMURA, Takeshi
;    APPLICANT:  KAWAGUCHI, Toshiya
;    APPLICANT:  KITAMURA, Naomi
     TITLE OF INVENTION:  NOVEL PROTEIN, DNA CODING FOR SAME
     TITLE OF INVENTION:  AND METHOD OF PRODUCING THE PROTEIN
     NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,196
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/685,660
;      FILING DATE:  24-JUL-1996
;      APPLICATION NUMBER:  JPA Hei 7-187134
;      FILING DATE:  24-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  Q-42295
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  252 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-974-196-7


  Query Match           100.0%;  Score 170;  DB 2;  Length 252;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-150;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
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Db      88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 197


RESULT   3
US-08-685-660A-3
; Sequence 3, Application US/08685660A
; Patent No. 5731412
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMOMURA, Takeshi
;    APPLICANT:  KAWAGUCHI, Toshiya
;    APPLICANT:  KITAMURA, Naomi
;    TITLE OF INVENTION:  NOVEL PROTEIN, DNA CODING FOR SAME
;    TITLE OF INVENTION:  AND METHOD OF PRODUCING THE PROTEIN
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/685,660A
;      FILING DATE:  24-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JPA Hei 7-187134
;      FILING DATE:  24-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  Q-42295
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal fragment
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      STRAIN:  MKN45
US-08-685-660A-3


  Query Match           15.3%;  Score 26;  DB 1;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      62 ATVTENATGDLATSRNAADSSVPSAP 87
           ||||||||||||||||||||||||||
Db       1 ATVTENATGDLATSRNAADSSVPSAP 26


RESULT   4
US-08-974-196-3
; Sequence 3, Application US/08974196
; Patent No. 5854396
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMOMURA, Takeshi
;    APPLICANT:  KAWAGUCHI, Toshiya
;    APPLICANT:  KITAMURA, Naomi
;    TITLE OF INVENTION:  NOVEL PROTEIN, DNA CODING FOR SAME
;    TITLE OF INVENTION:  AND METHOD OF PRODUCING THE PROTEIN
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
```

```
;       STREET:  2100 Pennsylvania Avenue, N.W.
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20037
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy Disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/974,196
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/685,660
;       FILING DATE:  24-JUL-1996
;       APPLICATION NUMBER:  JPA Hei 7-187134
;       FILING DATE:  24-JUL-1995
      ATTORNEY/AGENT INFORMATION:
        NAME:  KIT, Gordon
        REGISTRATION NUMBER:  30,764
;       REFERENCE/DOCKET NUMBER:  Q-42295
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 293-7060
;       TELEFAX:  (202) 293-7860
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  26 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal fragment
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;       STRAIN:  MKN45
US-08-974-196-3


  Query Match             15.3%;  Score 26;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      62 ATVTENATGDLATSRNAADSSVPSAP 87
           ||||||||||||||||||||||||||
Db       1 ATVTENATGDLATSRNAADSSVPSAP 26


  SULT   5
  -08-685-660A-2
  Sequence 2, Application US/08685660A
; Patent No. 5731412
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMOMURA, Takeshi
;    APPLICANT:  KAWAGUCHI, Toshiya
;    APPLICANT:  KITAMURA, Naomi
;    TITLE OF INVENTION:  NOVEL PROTEIN, DNA CODING FOR SAME
;    TITLE OF INVENTION:  AND METHOD OF PRODUCING THE PROTEIN
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/685,660A
;      FILING DATE:  24-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JPA Hei 7-187134
;      FILING DATE:  24-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  Q-42295
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal fragment
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      STRAIN:  MKN45
US-08-685-660A-2


  Query Match             8.8%;  Score 15;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps

Qy      21 RASMPRWWYNVTDGS 35
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Db       7 RASMPRWWYNVTDGS 21


RESULT   6
US-08-974-196-2
; Sequence 2, Application US/08974196
; Patent No. 5854396
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMOMURA, Takeshi
;    APPLICANT:  KAWAGUCHI, Toshiya
;    APPLICANT:  KITAMURA, Naomi
;    TITLE OF INVENTION:  NOVEL PROTEIN, DNA CODING FOR SAME
;    TITLE OF INVENTION:  AND METHOD OF PRODUCING THE PROTEIN
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,196
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/685,660
;      FILING DATE:  24-JUL-1996
;      APPLICATION NUMBER:  JPA Hei 7-187134
;      FILING DATE:  24-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  Q-42295
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 amino acids
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;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal fragment
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;       STRAIN:  MKN45
US-08-974-196-2


  Query Match             8.8%;  Score 15;  DB 2;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 RASMPRWWYNVTDGS 35
           |||||||||||||||
Db       7 RASMPRWWYNVTDGS 21


RESULT   7
US-08-685-660A-1
; Sequence 1, Application US/08685660A
; Patent No. 5731412
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMOMURA, Takeshi
;    APPLICANT:  KAWAGUCHI, Toshiya
;    APPLICANT:  KITAMURA, Naomi
;    TITLE OF INVENTION:  NOVEL PROTEIN, DNA CODING FOR SAME
;    TITLE OF INVENTION:  AND METHOD OF PRODUCING THE PROTEIN
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/685,660A
;      FILING DATE:  24-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JPA Hei 7-187134
;      FILING DATE:  24-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  Q-42295
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  N-terminal fragment
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      STRAIN:  MKN45
US-08-685-660A-1


  Query Match             5.9%;  Score 10;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0053;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDF 10
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Db       1 ADRERSIHDF 10


RESULT   8
US-08-974-196-1
; Sequence 1, Application US/08974196
; Patent No. 5854396
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMOMURA, Takeshi
;    APPLICANT:  KAWAGUCHI, Toshiya
;    APPLICANT:  KITAMURA, Naomi
;    TITLE OF INVENTION:  NOVEL PROTEIN, DNA CODING FOR SAME
;    TITLE OF INVENTION:  AND METHOD OF PRODUCING THE PROTEIN
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,196
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/685,660
;      FILING DATE:  24-JUL-1996
;      APPLICATION NUMBER:  JPA Hei 7-187134
;      FILING DATE:  24-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIT, Gordon
;      REGISTRATION NUMBER:  30,764
;      REFERENCE/DOCKET NUMBER:  Q-42295
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  N-terminal fragment
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      STRAIN:  MKN45
US-08-974-196-1


  Query Match             5.9%;  Score 10;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0053;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDF 10
           ||||||||||
Db       1 ADRERSIHDF 10


RESULT   9
US-08-676-124-93
; Sequence 93, Application US/08676124
; Patent No. 6010880
;  GENERAL INFORMATION:
;    APPLICANT:  MARKLAND, William
;    APPLICANT:  LADNER, Robert Charles
;    TITLE OF INVENTION:  INHIBITORS OF HUMAN PLASMIN DERIVED
;    TITLE OF INVENTION:  FROM FROM THE KUNITZ DOMIANS
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;    NUMBER OF SEQUENCES:  137
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/676,124
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
       APPLICATION NUMBER:  PCT/US95/00298
       FILING DATE:  11-JAN-1995
     PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/179,658
;      FILING DATE:  11-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/208,265
;      FILING DATE:  10-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  MARKLAND=3B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  93:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  58 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-676-124-93


  Query Match             5.9%;  Score 10;  DB 3;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    113 GPCRASFPRW 122
          ||||||||||
Db     12 GPCRASFPRW 21


RESULT  10
US-08-676-124-103
; Sequence 103, Application US/08676124
; Patent No. 6010880
;  GENERAL INFORMATION:
;    APPLICANT:  MARKLAND, William
;    APPLICANT:  LADNER, Robert Charles
;    TITLE OF INVENTION:  INHIBITORS OF HUMAN PLASMIN DERIVED
;    TITLE OF INVENTION:  FROM FROM THE KUNITZ DOMIANS
;    NUMBER OF SEQUENCES:  137
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/676,124
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00298
;      FILING DATE:  11-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/179,658
;      FILING DATE:  11-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/208,265
;      FILING DATE:  10-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  MARKLAND=3B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  103:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  58 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-676-124-103


  Query Match             5.9%;  Score 10;  DB 3;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    112 TGPCRASFPR 121
          ||||||||||
Db     11 TGPCRASFPR 20


RESULT  11
US-09-414-878-93
; Sequence 93, Application US/09414878
; Patent No. 6071723
;  GENERAL INFORMATION:
;    APPLICANT:  DYAX CORP
;    APPLICANT:  MARKLAND, William
;    APPLICANT:  LADNER,Robert C
;    TITLE OF INVENTION:  Inhibitors of Human Plamin Derived
;    TITLE OF INVENTION:  From The Kunitz Domains
;    NUMBER OF SEQUENCES:  139
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yankwich & Associates
;      STREET:  130 Bishop Allen Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02139
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5-inch diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Microsoft Word 97 SR-1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/414,878
;      FILING DATE:  (concurrently herewith)
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/240,136
;      FILING DATE:  29-JAN-1999
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/676,124
;      FILING DATE:  07-JAN-1997
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-414-878-93

Query Match 5.9%; Score 10; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 GPCRASFPRW 122
||||||||||
Db 12 GPCRASFPRW 21

RESULT 12
US-09-414-878-103
; Sequence 103, Application US/09414878
; Patent No. 6071723
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER,Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/414,878
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/240,136
; FILING DATE: 29-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-414-878-103

Query Match 5.9%; Score 10; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 TGPCRASFPR 121
||||||||||
Db 11 TGPCRASFPR 20

RESULT 13
US-09-240-136-93
; Sequence 93, Application US/09240136
; Patent No. 6103499
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER,Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,136
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994

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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, Leon R
;      REGISTRATION NUMBER:  30,237
;      NAME:  ZWICKER, Kenneth P
;      REGISTRATION NUMBER:  43,310
;      REFERENCE/DOCKET NUMBER:  DYX-007.2P US-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-491-4343
;      TELEFAX:  617-491-8801
;  INFORMATION FOR SEQ ID NO:  93:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  58 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-240-136-93


 Query Match             5.9%;  Score 10;  DB 3;  Length 58;
 Best Local Similarity   100.0%;  Pred. No. 0.016;
 Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     113 GPCRASFPRW 122
           ||||||||||
Db      12 GPCRASFPRW 21


RESULT  14
US-09-240-136-103
; Sequence 103, Application US/09240136
; Patent No. 6103499
;  GENERAL INFORMATION:
;    APPLICANT:  DYAX CORP
;    APPLICANT:  MARKLAND, William
;    APPLICANT:  LADNER,Robert C
;    TITLE OF INVENTION:  Inhibitors of Human Plamin Derived
;    TITLE OF INVENTION:  From The Kunitz Domains
;    NUMBER OF SEQUENCES:  139
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yankwich & Associates
;      STREET:  130 Bishop Allen Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02139
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5-inch diskette
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Microsoft Word 97 SR-1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/240,136
;      FILING DATE:  (concurrently herewith)
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/676,124
;      FILING DATE:  07-JAN-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00298
;      FILING DATE:  11-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,265
;      FILING DATE:  10-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/179,685
;      FILING DATE:  11-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, Leon R
;      REGISTRATION NUMBER:  30,237
;      NAME:  ZWICKER, Kenneth P
;      REGISTRATION NUMBER:  43,310
;      REFERENCE/DOCKET NUMBER:  DYX-007.2P US-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-491-4343
;      TELEFAX:  617-491-8801
;  INFORMATION FOR SEQ ID NO:  103:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  58 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-240-136-103


 Query Match             5.9%;  Score 10;  DB 3;  Length 58;
 Best Local Similarity   100.0%;  Pred. No. 0.016;
 Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps

Qy     112 TGPCRASFPR 121
           ||||||||||
Db      11 TGPCRASFPR 20


RESULT  15
US-08-358-160-116
; Sequence 116, Application US/08358160
; Patent No. 5663143
;  GENERAL INFORMATION:
;    APPLICANT:  LEY, Arthur C.
;    APPLICANT:  LADNER, Robert C.
;    APPLICANT:  GUTERMAN, Sonia K.
;    APPLICANT:  ROBERTS, Bruce L.
;    APPLICANT:  MARKLAND, William
;    APPLICANT:  KENT, Rachel B.
;    TITLE OF INVENTION:  ENGINEERED HUMAN-DERIVED KUNITZ
;    TITLE OF INVENTION:  DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
;    NUMBER OF SEQUENCES:  234
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W. Suite 300
;      CITY:  Washington
;      STATE:  District of Columbia
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,160
;      FILING DATE:  16-DEC-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/133,031
;      FILING DATE:  13-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/009,319
;      FILING DATE:  26-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/664,989
;      FILING DATE:  01-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/487,063
;      FILING DATE:  02-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/240,160
;      FILING DATE:  02-SEP-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cooper, Iver P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  LEY=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
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; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-116

Query Match 5.3%; Score 9; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 FIYGGCRGN 142
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Db 35 FIYGGCRGN 43

Search completed: January 31, 2001, 15:06:02
Job time: 103 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 31, 2001, 15:04:16 ; Search time 16.78 Seconds
(without alignments)
346.421 Million cell updates/sec

Title: US-09-441-654A-1
Perfect score: 170
Sequence: 1 ADRERSIHDFCLVSKVVGRC.....ACMLRCFRQQENPPLPLGSK 170

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 268485 seqs, 34193795 residues

Word size : 0

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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15: /SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	100.0	170	18	W30041	Human placental bi
2	170	100.0	179	18	W30053	Human placental bi
3	170	100.0	197	18	W30043	Human placental bi
4	170	100.0	213	18	W30042	Human placental bi
5	170	100.0	225	18	W30046	Human placental bi
6	170	100.0	235	18	W30060	Human consensus bi
7	170	100.0	240	18	W30045	Human placental bi
8	170	100.0	248	18	W30044	Human consensus bi
9	170	100.0	252	18	W30040	Human placental bi
10	170	100.0	252	18	W13665	Hepatocyte growth
11	170	100.0	252	19	W70286	Human tissue facto
12	153	90.0	153	18	W30051	Human placental bi
13	146	85.9	146	18	W30052	Human placental bi
14	92	54.1	92	18	W30054	Human placental bi
15	84	49.4	169	18	W30063	EST R74593 protein
16	72	42.4	130	18	W30062	EST R35464 protein
17	58	34.1	58	18	W30047	Human placental bi
18	58	34.1	58	18	W30049	Human placental bi
19	51	30.0	51	18	W30048	Human placental bi
20	51	30.0	51	18	W30050	Human placental bi
21	38	22.4	170	18	W30061	Human consensus bi
22	26	15.3	26	18	W13664	Hepatocyte growth
23	15	8.8	29	18	W13663	Hepatocyte growth
24	11	6.5	302	14	R35001	LACI. Rattus rat
25	11	6.5	302	17	R88513	Lipoprotein-associ
26	10	5.9	12	16	R78576	LACI K1 derivative
27	10	5.9	12	16	R78586	LACI K1 derivative
28	10	5.9	15	18	W13662	Hepatocyte growth
29	9	5.3	12	16	R78594	LACI K1 derivative
30	8	4.7	12	16	R78579	LACI K1 derivative
31	8	4.7	58	18	W07766	Non-native Kunitz
32	8	4.7	58	19	W64138	Human Kunitz-type
33	8	4.7	219	21	Y54090	Enzyme EPSE involv
34	8	4.7	219	21	Y43792	Amino acid sequenc
35	7	4.1	12	16	R78578	LACI K1 derivative
36	7	4.1	56	14	R39677	C-terminal Kunitz-
37	7	4.1	57	11	R08293	Example of Alzheim
38	7	4.1	57	19	W47434	Aprotinin variant
39	7	4.1	57	19	W47435	Aprotinin variant
40	7	4.1	57	19	W47436	Aprotinin variant
41	7	4.1	57	21	Y68103	Kunitz protease in
42	7	4.1	58	14	R39673	C-terminal Kunitz-
43	7	4.1	58	14	R39799	Kunitz-type protea
44	7	4.1	58	14	R39800	Kunitz-type protea
45	7	4.1	58	16	R78556	Human ITI-KuDOM 2

ALIGNMENTS

RESULT 1
W30041
ID W30041 standard; Protein; 170 AA.
XX
AC W30041;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX

PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 65; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 170 AA;

Query Match 100.0%; Score 170; DB 18; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.4e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
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Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
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RESULT 2
W30053
W30053 standard; Protein; 179 AA.

AC W30053;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 67; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 179 AA;

Query Match 100.0%; Score 170; DB 18; Length 179;
Best Local Similarity 100.0%; Pred. No. 2.5e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps

```
Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 60

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 120

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 170
```

RESULT 3
W30043
ID W30043 standard; Protein; 197 AA.
XX
AC W30043;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX

PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 65; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 170; DB 18; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.7e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
Db 19 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 78

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
Db 79 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 138

Qy 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
Db 139 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 188

RESULT 4
W30042
ID W30042 standard; Protein; 213 AA.
XX
AC W30042;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 65; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 213 AA;

Query Match 100.0%; Score 170; DB 18; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
Db 1 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 60

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
Db 61 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 120

Qy 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
Db 121 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 170

RESULT 5
W30046
ID W30046 standard; Protein; 225 AA.

XX
AC W30046;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 66; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 170; DB 18; Length 225;
Best Local Similarity 100.0%; Pred. No. 3e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 60

Qy     61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 120

Qy    121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 170
```

RESULT 6
W30060
ID W30060 standard; Protein; 235 AA.
XX
AC W30060;
XX
DT 20-APR-1998 (first entry)
XX
DE Human consensus bikunin.
XX
KW Human; consensus bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 198
FT /note= "encoded by TGA"
FT Misc-difference 201
FT /note= "encoded by TGA"
FT Misc-difference 226
FT /note= "encoded by GAN"
FT Misc-difference 233
FT /note= "encoded by TGA"
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
DR N-PSDB; T90732.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Disclosure; Fig 3; 110pp; English.
XX
CC The present sequence is a consensus human bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor

CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 235 AA;

Query Match 100.0%; Score 170; DB 18; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.1e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 78

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 138

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     139 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 188
```

RESULT 7
W30045
ID W30045 standard; Protein; 240 AA.
XX
AC W30045;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
DR N-PSDB; T90734.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 66; 110pp; English.
XX
CC The present sequence is human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 240 AA;

Query Match 100.0%; Score 170; DB 18; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 197
```

RESULT 8
W30044
ID W30044 standard; Protein; 248 AA.
XX
AC W30044;
XX
DT 20-APR-1998 (first entry)
XX
DE Human consensus bikunin.
XX
KW Human; consensus bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
DR N-PSDB; T90733.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX

```
PS   Claim 1; Page 66; 110pp; English.
XX
CC   The present sequence is a consensus human bikunin, which
CC   inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC   Bikunin can be used to treat or prevent brain and spinal cord
CC   oedema, inflammation, infection or granulomatosis, multiple
CC   sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC   fibrosis, blood coagulation diseases, polytrauma, stroke,
CC   cerebral or subarachnoid haemorrhage and gastric or cervical
CC   cancer and prevent metastasis. It is particularly useful for
CC   reducing blood loss during surgery, and can also be used to treat
CC   other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC   influenza and similar viral infections, acute pancreatitis and
CC   gout, and prevent pre-term labour. It has similar properties to
CC   aprotinin, but is less highly charged so should be less
CC   immunogenic and less likely to damage the kidneys. Manipulation
CC   of the bikunin sequence may allow the inhibitory profile to be
CC   altered. It also reduces or eliminates the need for whole donor
CC   blood or blood products during surgery, thereby reducing the risk
CC   of infection and other adverse side effects, as well as reducing
CC   the cost of surgery.
XX
SQ   Sequence   248 AA;


  Query Match             100.0%;  Score 170;  DB 18;  Length 248;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-156;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 83

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      84 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 143

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     144 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 193


RESULT   9
W30040
ID   W30040 standard; Protein; 252 AA.
XX
AC   W30040;
XX
DT   20-APR-1998  (first entry)

DE   Human placental bikunin.
XX
KW   Human; placental bikunin; inhibition; trypsin; kallikrein;
KW   plasmin; factor XIIa; treatment; prevention; oedema;
KW   inflammation; infection; granulomatosis; multiple sclerosis;
KW   ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW   blood coagulation disease; polytrauma; stroke; haemorrhage;
KW   gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS   Homo sapiens.
XX
PN   WO9733996-A2.
XX
PD   18-SEP-1997.
XX
PF   10-MAR-1997;   97WO-US03894.
XX
PR   04-OCT-1996;   96US-0725251.
PR   11-MAR-1996;   96US-0013106.
PR   14-JUN-1996;   96US-0019793.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Davis G,  Delaria KA,  Marlor CW,  Muller DK,  Tamburini PP;
XX
DR   WPI; 1997-470876/43.
DR   N-PSDB; T90731.
XX
PT   New human placental bikunin - used to inhibit kallikrein, trypsin
PT   etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT   perioperative blood loss
XX
PS   Claim 1; Page 65; 110pp; English.
XX
CC   The present sequence is a human placental bikunin, which
CC   inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC   Bikunin can be used to treat or prevent brain and spinal cord
CC   oedema, inflammation, infection or granulomatosis, multiple
CC   sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC   fibrosis, blood coagulation diseases, polytrauma, stroke,
CC   cerebral or subarachnoid haemorrhage and gastric or cervical
CC   cancer and prevent metastasis. It is particularly useful for
CC   reducing blood loss during surgery, and can also be used to treat
CC   other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC   influenza and similar viral infections, acute pancreatitis and
CC   gout, and prevent pre-term labour. It has similar properties to
CC   aprotinin, but is less highly charged so should be less
CC   immunogenic and less likely to damage the kidneys. Manipulation
CC   of the bikunin sequence may allow the inhibitory profile to be
CC   altered. It also reduces or eliminates the need for whole donor
CC   blood or blood products during surgery, thereby reducing the risk
CC   of infection and other adverse side effects, as well as reducing
CC   the cost of surgery.
XX
SQ   Sequence   252 AA;


  Query Match             100.0%;  Score 170;  DB 18;  Length 252;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-156;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 197


RESULT  10
W13665
ID   W13665 standard; Protein; 252 AA.
XX
AC   W13665;
XX
DT   11-NOV-1997  (first entry)
XX
DE   Hepatocyte growth factor activator inhibitor HAI-II.
XX
KW   Hepatocyte growth factor activator inhibitor; HAI-II; HGF; human;
KW   protease inhibitor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= Sig_peptide
FT   Protein         28..252
FT                   /label= Mat_protein
XX
PN   EP758682-A2.
```

```
XX
PD   19-FEB-1997.
XX
PF   23-JUL-1996;   96EP-0111861.
XX
PR   24-JUL-1995;   95JP-0187134.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Kawaguchi T,  Kitamura N,  Shimomura T;
XX
DR   WPI; 1997-134770/13.
DR   N-PSDB; T61439.
XX
PT   Novel protein HAI-II - inhibits protease activity of hepatocyte
PT   growth factor activator
XX
PS   Claim 4; Page 18-19; 24pp; English.
XX
CC   This sequence comprises a novel protein, designated HAI-II,
CC   that inhibits the protease activity of hepatocyte growth factor
CC   (HGF) activator.  The sequence was deduced from a cDNA clone
CC   (T61439) obtained from cancer cell line MKN45.  Also claimed
CC   are isolated peptides (W13662-64) of HAI-II, the DNA encoding
CC   HAI-II, a vector carrying this DNA, and a host cell, pref. an
CC   animal cell, transformed with the vector.  HAI-II can be used for
CC   regulating HGF activator activity (and thus HGF activity) in vitro
CC   and in vivo.  It may also be used for investigating the function of
CC   HAI-II in vivo and the effect of HAI-II in hepatic disorders.
XX
SQ   Sequence   252 AA;


 Query Match             100.0%;  Score 170;  DB 18;  Length 252;
 Best Local Similarity   100.0%;  Pred. No. 3.3e-156;
 Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 87

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp 147

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 197


RESULT  11
W70286
ID   W70286 standard; Protein; 252 AA.
XX
AC   W70286;
XX
DT   06-NOV-1998  (first entry)
XX
DE   Human tissue factor pathway inhibitor-3 (TFPI-3).
XX
KW   Human tissue factor pathway inhibitor-3; TFPI-3; blood clot; sepsis;
KW   fibrin clot; coronary occlusion; acute myocardial infarction;
KW   prophylaxis; peripheral arterial embolism; inflammatory disease;
KW   transplant rejection; anticoagulant; blood transfusion;
KW   extracorporeal circulation; dialysis; haemophili; kunitz type domain.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /note= "Signal peptide"
FT   Protein         28..252
FT                   /note= "TFPI-3"
XX
PN   WO9833920-A2.
XX
PD   06-AUG-1998.
XX
PF   27-JAN-1998;   98WO-US01468.
XX
PR   31-JAN-1997;   97US-0036703.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Gentz RL,  Hsu T,  Ni J,  Rosen CA;
XX
DR   WPI; 1998-437473/37.
DR   N-PSDB; V33063.
XX
PT   Isolated tissue factor pathway inhibitor-3 - used to develop
PT   products for treating, e.g. pulmonary embolism, thrombosis, sepsis,
PT   inflammatory disease, transplant rejection or haemophilia
XX
PS   Disclosure; Fig 1A-1B; 57pp; English.
XX
CC   The present sequence represents a human tissue factor pathway
CC   inhibitor-3 (TFPI-3) which contains two kunitz type domains.  The
CC   invention also provides the TFPI-3 cDNA and screening methods for
CC   identifying agonists and antagonists of TFPI-3.  As TFPI-3 inhibits
CC   protease activity, it is claimed to be useful for, e.g. inhibiting
CC   intravascular clotting and preventing the formation of fibrin clots
CC   both in vitro and in vivo, for treating coronary occlusion with acute
CC   myocardial infarction and in the prophylaxis and treatment of
CC   peripheral arterial embolism, for the treatment of sepsis, inflammatory
CC   diseases and transplant rejection.  TFPI-3 is also claimed to be useful
CC   as an anticoagulant in blood transfusions, extracorporeal circulation,
CC   and dialysis procedures and in blood samples for laboratory purposes.
CC   The TFPI-3 antagonists are claimed to be useful for promoting
CC   coagulation, e.g. in the treatment of haemophilia.
XX
SQ   Sequence   252 AA;


  Query Match             100.0%;  Score 170;  DB 19;  Length 252;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-156;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFP
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 catvtenatgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfp

Qy     121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENPPLPLGSK 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 rwyfdvernscnnfiyggcrgnknsyrseeacmlrcfrqqenpplplgsk 197


RESULT  12
W30051
ID   W30051 standard; Protein; 153 AA.
XX
AC   W30051;
XX
DT   20-APR-1998  (first entry)
XX
DE   Human placental bikunin.
XX
KW   Human; placental bikunin; inhibition; trypsin; kallikrein;
KW   plasmin; factor XIIa; treatment; prevention; oedema;
KW   inflammation; infection; granulomatosis; multiple sclerosis;
KW   ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW   blood coagulation disease; polytrauma; stroke; haemorrhage;
KW   gastric cancer; cervical cancer; metastasis; blood loss.
```

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XX
OS   Homo sapiens.
XX
PN   WO9733996-A2.
XX
PD   18-SEP-1997.
XX
PF   10-MAR-1997;   97WO-US03894.
XX
PR   04-OCT-1996;   96US-0725251.
PR   11-MAR-1996;   96US-0013106.
PR   14-JUN-1996;   96US-0019793.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Davis G,  Delaria KA,  Marlor CW,  Muller DK,  Tamburini PP;
XX
DR   WPI; 1997-470876/43.
XX
PT   New human placental bikunin - used to inhibit kallikrein, trypsin
PT   etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT   perioperative blood loss
XX
PS   Claim 1; Page 67; 110pp; English.
XX
CC   The present sequence is a human placental bikunin, which
CC   inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC   Bikunin can be used to treat or prevent brain and spinal cord
CC   oedema, inflammation, infection or granulomatosis, multiple
CC   sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC   fibrosis, blood coagulation diseases, polytrauma, stroke,
CC   cerebral or subarachnoid haemorrhage and gastric or cervical
CC   cancer and prevent metastasis. It is particularly useful for
CC   reducing blood loss during surgery, and can also be used to treat
CC   other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC   influenza and similar viral infections, acute pancreatitis and
CC   gout, and prevent pre-term labour. It has similar properties to
CC   aprotinin, but is less highly charged so should be less
CC   immunogenic and less likely to damage the kidneys. Manipulation
CC   of the bikunin sequence may allow the inhibitory profile to be
CC   altered. It also reduces or eliminates the need for whole donor
CC   blood or blood products during surgery, thereby reducing the risk
CC   of infection and other adverse side effects, as well as reducing
CC   the cost of surgery.
XX
SQ   Sequence   153 AA;

  Query Match             90.0%;  Score 153;  DB 18;  Length 153;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-140;
  Matches  153;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       7 IHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTE 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkkcatvte 60

Qy      67 NATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDV 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 natgdlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfprwyfdv 120

Qy     127 ERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQ 159
          |||||||||||||||||||||||||||||||
Db     121 ernscnnfiyggcrgnknsyrseeacmlrcfrq 153


RESULT  13
W30052
ID   W30052 standard; Protein; 146 AA.
XX
AC   W30052;
XX
DT   20-APR-1998  (first entry)
XX
DE   Human placental bikunin.
XX
KW   Human; placental bikunin; inhibition; trypsin; kallikrein;
KW   plasmin; factor XIIa; treatment; prevention; oedema;
KW   inflammation; infection; granulomatosis; multiple sclerosis;
KW   ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW   blood coagulation disease; polytrauma; stroke; haemorrhage;
KW   gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS   Homo sapiens.
XX
PN   WO9733996-A2.
XX
PD   18-SEP-1997.
XX
PF   10-MAR-1997;   97WO-US03894.
XX
PR   04-OCT-1996;   96US-0725251.
PR   11-MAR-1996;   96US-0013106.
PR   14-JUN-1996;   96US-0019793.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Davis G,  Delaria KA,  Marlor CW,  Muller DK,  Tamburini PP;
XX
DR   WPI; 1997-470876/43.
XX
PT   New human placental bikunin - used to inhibit kallikrein, trypsin
PT   etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT   perioperative blood loss
XX
PS   Claim 1; Page 67; 110pp; English.
XX
CC   The present sequence is a human placental bikunin, which
CC   inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC   Bikunin can be used to treat or prevent brain and spinal cord
CC   oedema, inflammation, infection or granulomatosis, multiple
CC   sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC   fibrosis, blood coagulation diseases, polytrauma, stroke,
CC   cerebral or subarachnoid haemorrhage and gastric or cervical
CC   cancer and prevent metastasis. It is particularly useful for
CC   reducing blood loss during surgery, and can also be used to treat
CC   other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC   influenza and similar viral infections, acute pancreatitis and
CC   gout, and prevent pre-term labour. It has similar properties to
CC   aprotinin, but is less highly charged so should be less
CC   immunogenic and less likely to damage the kidneys. Manipulation
CC   of the bikunin sequence may allow the inhibitory profile to be
CC   altered. It also reduces or eliminates the need for whole donor
CC   blood or blood products during surgery, thereby reducing the risk
CC   of infection and other adverse side effects, as well as reducing
CC   the cost of surgery.
XX
SQ   Sequence   146 AA;

  Query Match             85.9%;  Score 146;  DB 18;  Length 146;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-133;
  Matches  146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 CLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKKCATVTENATG 70
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 clvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkkcatvtenatg 60

Qy      71 DLATSRNAADSSVPSAPRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVERNS 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 dlatsrnaadssvpsaprrqdsedhssdmfnyeeyctanavtgpcrasfprwyfdverns 120

Qy     131 CNNFIYGGCRGNKNSYRSEEACMLRC 156
           |||||||||||||||||||||||||
Db     121 cnnfiyggcrgnknsyrseeacmlrc 146
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RESULT  14
W30054
ID   W30054 standard; Protein; 92 AA.
XX
AC   W30054;
XX
DT   20-APR-1998  (first entry)
XX
DE   Human placental bikunin.
XX
KW   Human; placental bikunin; inhibition; trypsin; kallikrein;
KW   plasmin; factor XIIa; treatment; prevention; oedema;
KW   inflammation; infection; granulomatosis; multiple sclerosis;
KW   ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW   blood coagulation disease; polytrauma; stroke; haemorrhage;
KW   gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS   Homo sapiens.
XX
PN   WO9733996-A2.
XX
PD   18-SEP-1997.
XX
PF   10-MAR-1997;   97WO-US03894.
XX
PR   04-OCT-1996;   96US-0725251.
PR   11-MAR-1996;   96US-0013106.
PR   14-JUN-1996;   96US-0019793.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Davis G,  Delaria KA,  Marlor CW,  Muller DK,  Tamburini PP;
XX
DR   WPI; 1997-470876/43.
XX
PT   New human placental bikunin - used to inhibit kallikrein, trypsin
PT   etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT   perioperative blood loss
XX
PS   Claim 1; Page 67; 110pp; English.
XX
CC   The present sequence is a human placental bikunin, which
CC   inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC   Bikunin can be used to treat or prevent brain and spinal cord
CC   oedema, inflammation, infection or granulomatosis, multiple
CC   sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC   fibrosis, blood coagulation diseases, polytrauma, stroke,
CC   cerebral or subarachnoid haemorrhage and gastric or cervical
CC   cancer and prevent metastasis. It is particularly useful for
CC   reducing blood loss during surgery, and can also be used to treat
CC   other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC   influenza and similar viral infections, acute pancreatitis and
CC   gout, and prevent pre-term labour. It has similar properties to
CC   aprotinin, but is less highly charged so should be less
CC   immunogenic and less likely to damage the kidneys. Manipulation
CC   of the bikunin sequence may allow the inhibitory profile to be
CC   altered. It also reduces or eliminates the need for whole donor
CC   blood or blood products during surgery, thereby reducing the risk
CC   of infection and other adverse side effects, as well as reducing
CC   the cost of surgery.
XX
SQ   Sequence   92 AA;

  Query Match             54.1%;  Score 92;  DB 18;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-81;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 adrersihdfclvskvvgrcrasmprwwynvtdgscqlfvyggcdgnsnnyltkeeclkk 60

Qy      61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
           |||||||||||||||||||||||||||||||
Db      61 catvtenatgdlatsrnaadssvpsaprrqds 92


RESULT  15
W30063
ID   W30063 standard; Protein; 169 AA.
XX
AC   W30063;
XX
DT   20-APR-1998  (first entry)
XX
DE   EST R74593 protein.
XX
KW   Human; consensus bikunin; inhibition; trypsin; kallikrein;
KW   plasmin; factor XIIa; treatment; prevention; oedema;
KW   inflammation; infection; granulomatosis; multiple sclerosis;
KW   ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW   blood coagulation disease; polytrauma; stroke; haemorrhage;
KW   gastric cancer; cervical cancer; metastasis; blood loss;
KW   EST R74593.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /note= "encoded by TAA"
FT   Misc-difference 23
FT                   /note= "encoded by TGA"
FT   Misc-difference 132
FT                   /note= "encoded by TGA"
FT   Misc-difference 135
FT                   /note= "encoded by TGA"
FT   Misc-difference 160
FT                   /note= "encoded by GAN"
FT   Misc-difference 167
FT                   /note= "encoded by TGA"
XX
PN   WO9733996-A2.
XX
PD   18-SEP-1997.
XX
PF   10-MAR-1997;   97WO-US03894.
XX
PR   04-OCT-1996;   96US-0725251.
PR   11-MAR-1996;   96US-0013106.
PR   14-JUN-1996;   96US-0019793.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Davis G,  Delaria KA,  Marlor CW,  Muller DK,  Tamburini PP;
XX
DR   WPI; 1997-470876/43.
DR   N-PSDB; T90736.
XX
PT   New human placental bikunin - used to inhibit kallikrein, trypsin
PT   etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT   perioperative blood loss
XX
PS   Disclosure; Fig. 2; 110pp; English.
XX
CC   The present sequence is the EST R74593 protein, which is similar
CC   to human bikunin. Bikunin inhibits, e.g. trypsin, kallikrein,
CC   plasmin and factor XIIa.
CC   Bikunin can be used to treat or prevent brain and spinal cord
CC   oedema, inflammation, infection or granulomatosis, multiple
CC   sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC   fibrosis, blood coagulation diseases, polytrauma, stroke,
CC   cerebral or subarachnoid haemorrhage and gastric or cervical
CC   cancer and prevent metastasis. It is particularly useful for
CC   reducing blood loss during surgery, and can also be used to treat
CC   other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC   influenza and similar viral infections, acute pancreatitis and
```

CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 169 AA;

Query Match 49.4%; Score 84; DB 18; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.6e-73;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      87 PRRQDSEDHSSDMFNYEEYCTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSY 146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39 prrqdsedhssdmfnyeeyctanavtgpcrasfprwyfdvernscnnfiyggcrgnknsy 98

      147 RSEEACMLRCFRQQENPPLPLGSK 170
          ||||||||||||||||||||||||
Db     99 rseeacmlrcfrqqenpplplgsk 122
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Search completed: January 31, 2001, 15:05:43
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